

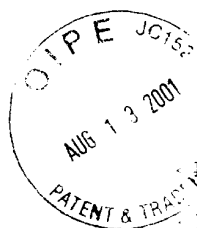
SEQUENCE LISTING

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<130> G-Superfamily Conotoxin Peptides

<140> 2314-227

<141> US 60/749,637

<142> 2000-11-29

<143> US 60/243,412

<144> 2000-10-27

<145> US60/119,440

<146> 2000-07-30

<147> US 60/114,263

<148> 2000-06-26

<149> US 60/173,754

<150> 1999-11-30

<151> 409

<152> PatentIn version 3.0

<153> 1

<154> 261

<155> BWA

<156> Venus gloriamaris

<157>

<158> CDS

<159> (1)...(31)

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 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala 15
 1 5 10

tta ara ttc gtc acg gct gat gac tcc gga aat gga atg gag att ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu 30
 25

tta cgg aag gag ggt cac gaa atg gag aac ctc gaa gtc tct aat cgg 144
 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg 45
 35 40

tta aag aca tgc cgt aaa gaa ggt aca ctt tgt gat cgg ata ttt caa 192
 Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln 60
 50 55 60

tta tgc ttc cgt ggc tgg aat tgc gtt ctt ttc tgc gtc tgaaactacc 241
 Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val 75
 65 70

gtatattttt ctctcccttc

<210> 1
<211> 17
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<213> Conus gloriamaris

<400> 3
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
20 25 30
Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
35 40 45
Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
50 55 60
Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val
65 70 75

<210> 3
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<212> PPT
<213> Conus gloriamaris

<400> 3
<210> SITE
<211> (1)..(19)
<212> Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residue
e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Trp
or bromo-Trp

<400> 3
Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
1 5 10 15
Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val
20 25

<210> 4
<211> 19
<212> PPT
<213> Conus gloriamaris

<400> 4
<210> SITE
<211> (1)..(19)
<212> Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residu
e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 15 may be Tyr
, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosphn
o-Tyr; Xaa at residue 12 may be Trp or bromo-Trp

<400> 4
Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Xaa Gln
1 5 10 15
Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val
20 25

<210> 5
<211> 29

<210> PRT
 <211> Conus gloriamaris

<212>
 <213> SITE
 <214> (1)..(29)
 <215> Xaa at residues 3 and 12 may be pro or hydroxy-Pro; Xaa at residue
 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp
 or bromo-Trp; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo
 -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 6
 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
 1 5 10 15
 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Xaa Cys Val
 20 25

<210> 6
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 <213> Conus omaria

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 tcatctgttc catcatatca ttcattcatt cgttcgcaga ctataataaa cattcaagtc 120
 tctcttcttt ttgtgtcttg acaga tgc atc agg atg tgc cgt aga gaa gct 172
 Ser Ile Arg Met Cys Arg Arg Glu Ala
 1 5
 gaa ctt tgt gat cgg att ttt caa aac tgc tgc cat ggc ttg ttt tgc 220
 Gln Leu Cys Asp Pro Ile Phe Gln Asn Cys Cys His Gly Leu Phe Cys
 10 15 20 25
 att ttg gtc tgc gtc taaaactacc gtgatgtctt ctctctccct ctagtagtag 275
 Val Leu Val Cys Val
 30
 tagggcgccg ctatagagga tccaagetta cgtacgggtg catgcgacgt catagctctt 335
 ctatagtgtc aactaaatto aattcaatgg cgttggtttt acaacgttgt gactgggaaa 395
 aacctgggtt taccgaactt aatgccttg cagcagatcc ccttttcgcc agctggcgta 455
 ctataggaaga ggccgcgacc gatgcgccctt cccaatagtt ggcgagcctg aatggcgaat 515
 gaaacgggcc ctgtagoggc gcattat 542

<210> 7
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 <212> PRT
 <213> Conus omaria

<400> 7
 Ser Ile Arg Met Cys Arg Arg Glu Ala Gln Leu Cys Asp Pro Ile Phe
 1 5 10 15
 Gln Asn Cys Cys His Gly Leu Phe Cys Val Leu Val Cys Val

20

25

30

<210> 8
 <211> 27
 <212> PPT
 <213> Conus omaria

<214>
 <215> SITE
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 <217> Xaa at residue 5 is Glu or gamma-carboxy-Glu; Xaa at residue 11 m
 ay be Pro or hydroxy-Pro

<218> A
 Met Cys Arg Arg Xaa Ala Gln Leu Cys Asp Xaa Ile Phe Gln Asn Cys
 1 5 10 15
 Cys His Gly Leu Phe Cys Val Leu Val Cys Val
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<219> A
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 <213> Conus textile

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 1 5
 ggt gtc ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gat gac tcc 99
 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser
 15 20 25
 gaa aat gga atg gag aat ctt ttt ccg aag gca ggt cac gaa atg gag 147
 Arg Asn Gly Met Glu Asn Leu Phe Pro Lys Ala Gly His Glu Met Glu
 30 35 40
 aac ctc gaa gac tct aaa cac agg cac cag gag aga ccg gac acc ggc 195
 Asn Leu Glu Asp Ser Lys His Arg His Gln Glu Arg Pro Asp Thr Gly
 45 50 55
 aac aaa gaa gag atg ctg cta cag aga cag gtc aag ccg tgt cgt aaa 243
 Asp Lys Glu Glu Met Leu Leu Gln Arg Gln Val Lys Pro Cys Arg Lys
 60 65 70
 gag cat caa ctt tgt gat ctg att ttt caa aac tgc tgc cgt ggc tgg 291
 Gln His Gln Leu Cys Asp Leu Ile Phe Gln Asn Cys Cys Arg Gly Trp
 75 80 85
 tat ttc gtt gtt ctg tct tgc act tgaaagctac ctgatgtgtt ctactcccat 345
 Tyr Cys Val Val Leu Ser Cys Thr
 90
 346

<210> 10
 <211> 27
 <212> PPT
 <213> Conus textile

<400> 10
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Trp Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Met Glu Asn Leu
 20 25 30
 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 35 40 45
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 50 55 60
 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
 65 70 75 80
 Ile Ile Gln Asn Cys Cys Arg Gly Trp Tyr Cys Val Val Leu Ser Cys
 85 90 95

Thr

<110> 11
 <111> 31
 <112> PBT
 <113> Conus textile

<110>
 <111> SITE
 <112> (1)..(31)
 <113> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residue 4 may be
 Pro or hydroxy-Pro; Xaa at residue 8 may be Glu or gamma-carboxy-
 Glu; Xaa at residue 23 may be Trp or bromo-Trp; Xaa at residue 24

<110>
 <111> SITE
 <112> (1)..(31)
 <113> may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 11
 Xaa Val Lys Xaa Cys Arg Lys Xaa His Gln Leu Cys Asp Leu Ile Phe
 1 5 10 15
 Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Val Val Leu Ser Cys Thr
 20 25 30

<110> 12
 <111> 265
 <112> DNA
 <113> Conus omaria

<110>
 <111> CDS
 <112> (1)..(234)

<400> 12
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 1 5 10 15
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Ser Leu Thr Gly
 20 25 30
 tpy aca ttc gtc acg gct gat gac ttt gga aat gga ttg gag aat ctt
 35 40 45 50 55 60
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu

48

96

ttt tgg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 45 40 45

aac aag agg tgc gtt cca cac gag ggc cct tgt aat tgg ctt aca caa 192
 Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln
 50 55 60

aat tgc tgc agt ggt tat aat tgc atc att ttt ttc tgc cta 234
 Asn Cys Cys Ser Gly Tyr Asn Cys Ile Ile Phe Phe Cys Leu
 65 70 75

taaaatcaccgtgatgtcttctcttccccc c 265

<110> 13
 <111> 78
 <112> PPT
 <113> Genus cmaria

<120> 13
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 1 5 10

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu 30
 20 25

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 45
 35 40

Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln 60
 45 55 60

Asn Cys Cys Ser Gly Tyr Asn Cys Ile Ile Phe Phe Cys Leu 75
 65 70

<110> 14
 <111> 27
 <112> PPT
 <113> Genus cmaria

<110>
 <111> SITE
 <112> (1)..(27)
 <113> Xaa at residues 3 and 7 may be Pro or hydroxy-Pro; Xaa at residue
 5 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Trp
 or bromo-Trp; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<120> 14
 Cys Val Xaa His Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys 15
 1 5 10

Ser Gly Xaa Asn Cys Ile Ile Phe Phe Cys Leu 25
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<110> 19
 <111> 241
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 <113> Genus calli

<110>
 <111> IDS
 <112> (1)..(291)

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 Met Lys Leu Thr Cys Leu Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg ara ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
 20 25 30
 ttt ccg aag gca cgt cac gaa atg gag aac ctg gaa gac tct aaa cac 144
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 35 40 45
 aga cag cag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 50 55 60
 cag aga cag gtc aag ccg tgt cgt aaa gaa cat caa ctt tgt gat ctg 240
 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
 65 70 75 80
 att att caa aac tgc tgc cgt ggc tgg tat tgc ttg ctt cgt cct tgc 288
 Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Leu Leu Arg Pro Cys
 85 90 95
 atc caaactacc ggcgtgtctt ctctccatc 321
 Ile

<110> 16
 <111> 97
 <112> FRT
 <113> Conus dalli

<400> 16
 Met Lys Leu Thr Cys Leu Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
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 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 35 40 45
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 50 55 60
 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
 65 70 75 80
 Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Leu Leu Arg Pro Cys
 85 90 95

Ile

<110> 17
 <111> 81
 <112> FRT
 <113> Conus dalli

<110>
 <111> SITE
 <112> (1)..
 <113> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 4 and 29
 may be Pro or hydroxy-Pro; Xaa at residue 8 may be Glu or gamma-

carboxy-Glu ; Xaa at residue 23 may be Trp or bromo-Trp;

<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residue 24 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 17

Xaa Val Lys Xaa Cys Arg Lys Xaa His Gln Leu Cys Asp Leu Ile Phe
1 5 10 15

Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Leu Leu Arg Xaa Cys Ile
20 25 30

<410> 18

<411> 321

<412> DNA

<413> *Conus dalli*

<420>

<421> CDS

<422> (1)..(291)

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1 5 10 15

tgt acc ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
20 25 30

att ccg aag aca cgt cac gaa atg gag aac ctc gaa gac tct aaa cac 144
Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
35 40 45

agg cac cag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192
Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
50 55 60

cag aga cgg gtc aag ccg tgc agt gaa gaa ggt caa ctt tgt gat cca 240
Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro
65 70 75 80

att tct caa aac tgc tgc cgt ggc tgg cat tgc gtt ctt gtc tct tgc 288
Leu Ser Gln Asn Cys Cys Arg Gly Trp His Cys Val Leu Val Ser Cys
85 90 95

atc tgaaactacc gtgatgtctt ctctccacc 321
Val

<410> 19

<411> 97

<412> PRT

<413> *Conus dalli*

<430> 19

Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
20 25 30

Phe Phe Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 35 40 45
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 50 55 60
 Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro
 65 70 75 80
 Leu Ser Gln Asn Cys Cys Arg Gly Trp His Cys Val Leu Val Ser Cys
 85 90 95

Val

0110 20
 0111 20
 0112 PPT
 0113 Genus dalli

0200
 0210 SITE
 0220 (1)..
 0230 Xaa at residues 3 and 13 may be Pro or hydroxy-Pro; Xaa at residue
 6 and 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 ma
 y be Trp or bromo-Trp

0400 20
 Val Lys Xaa Cys Ser Xaa Xaa Gly Gln Leu Cys Asp Xaa Leu Ser Gln
 1 5 10 15
 Asn Cys Cys Arg Gly Xaa His Cys Val Leu Val Ser Cys Val
 20 25 30

0100 11
 0110 406
 0120 DNA
 0130 Genus textile

0200
 0210 CDS
 0220 (14)..
 0230

0400 21
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 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu
 1 5 10

ttg ctg acc gcc tgg aca ttt gac acg gct gat gac ccc aga aat gga 97
 Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
 15 20 25

ttg gga aat ctt ttt tog aat gca cat cac gaa atg aag aac ccc gaa 145
 Leu Gly Asn Leu Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu
 30 35 40

ggc tct aaa ttg aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt 193
 Ala Ser Lys Leu Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys
 45 50 55 60

aat ttg tta gac caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc 241
 Asn Leu Leu Asp Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val
 65 70 75

tgc aca taaaactggc gtgatgtctt ctcttccct ctgtgtacc tggcttgatc 297

Cys Thr

tttgatggg gogtgtogtt caetgyttat gaaccccccc ccccccccc ccccccccc 357
 tgggtcttc tggagggttc ggggggttcaa catccaaata aagtgcacg 406

4100 21
 42110 78
 42110 PFT
 42130 Genus textile

4400 21
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

4100 23
 42110 27
 42110 PFT
 42130 Genus textile

4200
 4211 SITE
 4221 (1)..(27)
 4230 Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
 Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

4400 23
 Xaa Cys Lys Gln Asp Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
 1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
 20 25

4100 24
 4211 27
 4211 PFT
 4213 Genus textile

4200
 4211 SITE
 4221 (1)..(26)
 4230 Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
 Glu or gamma-carboxy-Glu; Xaa at residue 9 is Nle; Xaa at residue
 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T
 yr or O-phospho-Tyr

4400 24
 Xaa Cys Lys Gln Asp Gly Xaa Xaa Cys Asn Leu Leu Asp Gln Asn Cys
 1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

<110> 15
<111> 165
<112> DNA
<113> Conus magus

<110>
<111> CDS
<112> (1)..(234)

<400> 25
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1 5 10 15
tgc aga ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30
ttt tgg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45
aac aac ang tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60
aaa aac tgg tgc gac gcc tat tgc ata gta ctt gtc tgc aca 234
Ala Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

aaagactggc gtgatgtctt ctctccct 265

<110> 26
<111> 78
<112> PPT
<113> Conus magus

<400> 26
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1 5 10 15
tgc thr phe ala thr ala asp asp pro arg asn gly leu gly asn leu
20 25 30
phe ser asn ala his his glu met lys asn pro glu ala ser lys leu
35 40 45
asn lys arg trp cys lys gln ser gly glu met cys asn leu leu asp
50 55 60
ala asn cys cys asp gly tyr cys ile val leu val cys thr
65 70 75

<110> 17
<111> 17
<112> PPT
<113> Conus magus

<110>
<111> SITE
<112> (1)..(27)

<123> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<124> 17
Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

<110> 28
<111> 27
<112> IFT
<113> Conus textile

<125>
<126> SITE
<127> (1)..(27)
<128> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<129> 13
Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Phe Val Cys Thr
20 25

<110> 29
<111> 265
<112> LNA
<113> Conus distans

<129>
<130> SLS
<131> (1)..(234)

<132> 24
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1 5 10 15
tgc aca ttt gcc acg gct gat gac gcc aga aat gga ttg ggg aat ctt 96
Tyr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30
tgc tgc aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45
aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
Asn Lys Arg Tyr Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60
tgc aac tgc tgc gac gcc tat tcc ata gta ctt gtc tgc aca 234
Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75
tgaagctgcc gtgatgtett ctctccct c 265

<110> 30
<111> 78

<110> PPT
 <113> Conus distans

<400> 30
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Tip Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Tip Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60
 Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

<110> 31
 <111> 27
 <112> PPT
 <113> Conus distans

<400>
 <401> SITE
 <402> (1)..(27)
 <403> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
 Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 21
 Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
 1 5 10 15
 Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
 20 25

<110> 32
 <111> 165
 <112> DNA
 <113> Conus ammiralis

<400>
 <401> SDS
 <402> (1)..(234)

<400> 32
 atg aag ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
 Tip Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30
 ... tgg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aat aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
 Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60

caa aac tgc tgc gag ggc tat tgc ata gta ctt gtc tgc aca
 Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

234

tataatgca gtgatgtctt ctctccct c

265

<110> 33

<111> 78

<112> PFT

<113> Conus ammiralis

<400> 33

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60

Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

<110> 34

<111> 27

<112> PFT

<113> Conus ammiralis

<114>

<115> SITE

<116> (1)..(27)

<117> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 7 and 1
 8 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr,
 1,5-di-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
 -Tyr

<400> 34

Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
 1 5 10 15

Cys Xaa Gly Xaa Cys Ile Val Leu Val Cys Thr
 20 25

<110> 35

<111> 156

<112> DNA

<113> Conus dalli

<114>

<115> CDS

<116> (1)..(215)

<400> 35

arg aac ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc
 5 10 15
 Gln Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala

48

arg aca ttc gtc acg gct gat gac ccc aga aat gga ttg gag aat ctt
 20 25 30
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu

96

ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct aag ttg aat 144
 Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
 35 40 45

gaa aag tgc ctt ggt ggt ggt gaa gtt tgt gat atc ttt ttt cca caa 192
 Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln
 55 60

tgt tgt ggc tat tgc att ctt ctt ttc tgc aca taaaactacc gtgatgtctt 245
 Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr
 65 70 75

gtgatgtctt c 256

4110 36
 4111 75
 4112 PPT
 4113 Conus dalli

4400 36
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Tyr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30

Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
 35 40 45

Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln
 50 55 60

Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr
 65 70 75

4110 37
 4111 75
 4112 PPT
 4113 Conus dalli

4110
 4111 SITE
 4112 (1)..(25)
 4113 Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-
 Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

4400 37
 Cys Leu Gly Gly Gly Xaa Val Cys Asp Ile Phe Phe Xaa Gln Cys Cys
 1 5 10 15

Gly Xaa Cys Ile Leu Leu Phe Cys Thr
 20 25

4110 38
 4111 441
 4112 tNA
 4113 Conus gloriamaris

4110
 4111 CES
 4112 (70)..(300)

4400 38

gcttgacagg tgaatttggc ttcacagttt ttcactgtcg tctttggcat catctgaaac 60
 atcqpaaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg 111
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu
 1 10
 acc ggc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 159
 Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly
 11 25 30
 aat att tit tgg aat gca cat cac gaa atg aag aat ccc gaa gcc tct 207
 Asn Ile Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser
 35 40 45
 aaa ttg aac aag aag tgc cgt cta ggc gct gaa agt tgt gat gta att 255
 Lys Leu Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile
 50 55 60
 tca caa aac tgc tgc caa ggc acg tgc gtt ttt ttc tgc tta cca 300
 Ser Gln Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro
 65 70 75
 tgaigtcttc taattctctc tgtgtacct ggcttgatct ttcattagcg cgtgccttcc 360
 acgtattatg aacccctga tccgactctc tggcagctc ggggggtcaa catccaaata 420
 aaacacagc acaatgacaa a 441

<210> 39
 <211> 77
 <212> PRT
 <213> Conus gloriamaris

<400> 39
 Met Lys Ieu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Ile
 20 25 30
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile Ser Gln
 50 55 60
 Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro
 65 70 75

<210> 40
 <211> 26
 <212> PRT
 <213> Conus gloriamaris

<210>
 <211> SITE
 <212> (1)..(26)
 <213> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 26 may be Pro or hydroxy-Pro

<400> 40
 Cys Arg Leu Gly Ala Xaa Ser Cys Asp Val Ile Ser Gln Asn Cys Cys
 1 5 10 15

Gln Gly Thr Cys Val Phe Phe Cys Leu Xaa
20 25

<210> 41
<211> 446
<212> DNA
<213> *Conus gloriamaris*

<214>
<215> CDS
<216> (74)..(304)

<430> 41
ggatccttgc acggtgaatt tggttcaca gttttccact gtgtgttttc gcatcatcca 60
aagcctacc aag atg aaa ctg aag tgc atg atg atc gtt gct gtg ctg 109
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu 10
1 5
ttt ttg acc gcc tgg aca ttc gcc acg gct gat gac ccc aga aat gga 157
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly 25
15 20
ttg gag aaa ctt ttt tgg aat aca cat cac gaa atg aag aac ccc gaa 205
Leu Gln Lys Leu Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu 40
30 35
ggt tct aaa ttg aac aag agg tgc aaa caa gct gat gaa tct tgt aat 253
Ala Ser Lys Leu Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn 60
40 50 55
gta ttt caa ctt gac tgc tgc acc ggc tta tgc ttg gga ttc tgc gta 301
Val Phe Ser Leu Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val 75
65 70
ctg tcatgtcttc tactcccttc tgtgtacct ggtttgatct ttgattggcg 354
Ser
tgtgcctttc atcgggttatg aacccccctg atccgattct ttggcggcct cgggggttca 414
acatccaaat aaagcgacag cacaataaaa aa 446

<210> 42
<211> 77
<212> PPT
<213> *Conus gloriamaris*

<400> 42
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala 15
1 5 10
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Lys Leu 30
20 25
Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 45
35 40
Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn Val Phe Ser Leu 60
50 55
Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val Ser 75
65 70

<410> 43
 <411> 26
 <412> EFT
 <413> Genus gloriamaris

<414>
 <415> SITE
 <416> (1)..(26)
 <417> Xaa at residue 6 may be Glu or gamma-carboxy-Glu.

<418> 43
 Cys Lys Gln Ala Asp Xaa Ser Cys Asn Val Phe Ser Leu Asp Cys Cys
 1 5 10 15

Thr Gly Leu Cys Leu Gly Phe Cys Val Ser
 20 25

<419> 44
 <420> 142
 <421> DNA
 <422> Genus gloriamaris

<423>
 <424> CDS
 <425> (1)..(225)

<426> 44
 arg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc acc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15

thr aaa ttc gcc acg gcc atc acc agg aat gga ttg ggg aat ctt ttt 96
 Thr Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe
 20 25 30

arg aag aat cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg aac 144
 Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn
 35 40 45

arg agg tgc gtt cca tac gag ggc cct tgt aat tgg ctt aca caa aac 192
 Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn
 50 55 60

tgt tgc gat gag cta tgc gta ttt ttc tgc cta taaaactagc ctgatgt 242
 Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu
 65 70 75

<427> 45
 <428> 75
 <429> EFT
 <430> Genus gloriamaris

<431> 45
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15

Thr Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe
 20 25 30

Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn
 35 40 45

Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn
 50 55 60

Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu
65 70 75

02100 46
0211 35
0212 PFT
0213 Conus gloriamaris

0220
0221 SITE
0222 (1)..(25)
0223 Xaa at residue 2 and 7 may be Pro or hydroxy-Pro; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 and 18 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Trp or bromo-Trp

0400 46
Cys Val Xaa Xaa Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys
1 5 10 15

Asp Xaa Leu Cys Val Phe Phe Cys Leu
20 25

0110 47
0111 150
0112 PNA
0113 Conus magus

0220
0221 CDS
0222 (1)..(231)

0400 47
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctc ttc ttg acc gtc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val 15
1 5 10
tgc aaa ttc gcc acg gct gat gac tcc gga aat gga ttg gag aaa ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu 30
20 25
ttt tgg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 45
25 40
aac aag aag tgc aaa gaa gct gat gaa cct tgt gat gta ttt toa ctt 192
Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu 60
50 55
gaa tgc tgc acc gcc ata tgt ctt gga ttc tgc acg tgg tgatgtcttc 241
Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp 75
65 70

ctacacctc 250

0110 48
0111 77
0112 PFT
0113 Conus magus

0400 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu
50 55 60

Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp
65 70 75

<110> 49

<111> 16

<112> FRT

<113> Conus magus

<120>

<121> SITE

<122> (71)..(26)

<123> Xaa at residue 6 and 14 may be Glu or gamma-carboxy-Glu; Xaa at r
residue 7 may be Pro or hydroxy-Pro; Xaa at residue 26 may be Trp o
r bromo-Trp

<130> 49

Cys Lys Gln Ala Asp Xaa Xaa Cys Asp Val Phe Ser Leu Xaa Cys Cys
1 5 10 15

Thr Gly Ile Cys Leu Gly Phe Cys Thr Xaa
20 25

<140> 50

<141> 424

<142> TGA

<143> Conus textile

<150>

<151> CDS

<152> (71)..(295)

<160> 50

gctttgcaag gtgaatttgg cttcatagtt ttccactgac gtctttggca tcatocaaaa 60

catcacaaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 109
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe
1 5 10

ttg acc gcc tgg aca ttc gcc acg gct gat gac tcc agc aat gga ttg 157
Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu
15 20 25

gag aat ctt ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct 205
Glu Asn Leu Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser
30 35 40 45

aag ttg aac gag agg tgc ctt gat gct ggt gaa gtt tgt gat att ttt 253
Lys Leu Asn Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe
50 55 60

tta cca aca tgc tgc ggc tat tgc att ctt ctt ttc tgc gca 295
Phe Pro Thr Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala
65 70 75

taaaaatacc gtgatgtctt ctatccctct ctgtgctacc tggettgtac tttgattggc 355

gagtagcatt cactgggttat gaaacccctg atccagctct ctggaggcct cgggggttca 415

asprcgaat aaagggaca 434

<110> 51
<111> 75
<112> PFT
<113> Conus textile

<400> 51
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu
20 25 30

Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
35 40 45

Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe Phe Pro Thr
50 55 60

Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala
65 70 75

<110> 51
<111> 20
<112> PFT
<113> Conus textile

<110> SITE
<111> (1)..(25)
<113> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
12 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-
I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

<400> 51
Cys Leu Asp Ala Gly Xaa Val Cys Asp Ile Phe Phe Xaa Thr Cys Cys
1 5 10 15

Gly Xaa Cys Ile Leu Leu Phe Cys Ala
20 25

<110> 53
<111> 20
<112> PFT
<113> Conus textile

<110> SITE
<111> (1)..(26)
<113> Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at r
residue 7 may be Pro or hydroxy-Pro

<400> 51
Cys Ile Xaa Gln Phe Asp Xaa Cys Xaa Met Ile Arg His Thr Cys Cys
1 5 10 15

Val Gly Val Cys Phe Leu Met Ala Cys Ile
20 25

<110> 54
<111> 26

<011> PPT
 <012> Genus textile

<020>
 <021> SITE
 <022> (1)..(26)
 <023> Xaa at residues 3, 7 and 13 may be Pro or hydroxy-Pro; Xaa at residue 14 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<030> 54
 Cys Ala Xaa Phe Leu His Xaa Cys Thr Phe Phe Phe Xaa Asn Cys Cys
 1 5 10 15

Asn Ser Xaa Cys Val Gln Phe Ile Cys Leu
 20 25

<010> 55
 <011> 260
 <012> DNA
 <013> Genus amaria

<010>
 <011> CDS
 <012> (1)..(140)

<030> 55
 atg aaa atg atg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gac atg gct gat gac ccc aga aat gga ttg gag aat ttt 96
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
 20 25 30
 ttt tgg aag ata caa cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag agg tgc cta gca gaa cat gaa act tgt aat ata ttt aca caa 192
 Asn Lys Arg Cys Leu Ala Glu His Glu Thr Cys Asn Ile Phe Thr Gln
 50 55 60
 aac tgc tgc gaa ggc gtg tgc att ttt atc tgc gta caa gct cca gag 240
 Asn Cys Cys Glu Gly Val Cys Ile Phe Ile Cys Val Gln Ala Pro Glu
 65 70 75 80

atatgtatttc tctctccctc 260

<010> 56
 <011> 89
 <012> PPT
 <013> Genus amaria

<030> 56
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
 20 25 30

Ile Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Cys Leu Ala Glu His Glu Thr Cys Asn Ile Phe Thr Gln
50 55 60

Asn Cys Cys Glu Gly Val Cys Ile Phe Ile Cys Val Gln Ala Pro Glu
65 70 75 80

1100 51

1110 19

1120 PRT

1130 Conus omaria

1140

1150 SITE

1160 (1)..(20)

1170 Xaa at residues 4, 6, 17 and 29 may be Glu or gamma-carboxy-Glu;
1180 Xaa at residue 28 may be Pro or hydroxy-Pro

1190 57

Cys Leu Ala Xaa His Xaa Thr Cys Asn Ile Phe Thr Gln Asn Cys Cys
1 5 10 15

Xaa Gly Val Cys Ile Phe Ile Cys Val Gln Ala Xaa Xaa
20 25

1120 58

1130 261

1140 DNA

1150 Conus omaria

1160

1170 CDS

1180 (1)..(231)

1190 58

atg aaa ctg act gtc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt acc acg gct gaa gac ccc aga cat gga ttg gag aat ctt 96
Tyr Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu
20 25 30

ttt tgg aag gca cat cac gaa atg aag aac cct gaa gac tct aaa ttg 144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
35 40 45

gac aag aag tgc att cca cat ttt gac cct tgt gac cag ata cgc cac 192
Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His
50 55 60

acc tac tgc ttt ggc ctg tgc cta cta ata gcc tgc atc taaaactgcc 241
Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
65 70 75

agatgttt ctctcccatc 261

1100 59

1110 77

1120 PFT

1130 Conus omaria

1140 59

Met Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu
 20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
 35 40 45

Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His
 50 55 60

Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 65 70 75

0110 60

0111 20

0112 PPT

0113 Conus omaria

0120

0121 SITE

0122 (1) (26)

0123 Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.

0400 60

Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys
 1 5 10 15

Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 20 25

0110 61

0111 159

0112 ENA

0113 Conus omaria

0120

0121 CDS

0122 (1) (228)

0400 61

atg aag ctg aag tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aag ttc atc aag gct gaa gac ccc aga gat gga ttg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu
 20 25 30

tta tca aat gca cat aac gaa atg aag aac ccc gaa gcc tct aca ttg 144
 Leu Ser Asn Ala His Asn Glu Met Lys Asn Pro Glu Ala Ser Thr Leu
 35 40 45

atc gaa agg tgc ctt ggg ttt ggt gaa gct tgt ctt ata ctt tat tca 192
 Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Ile Leu Tyr Ser
 50 55 60

atc ttc tgc ggc tat tgc gtt ggt gct atc tgc cta taaaactacc 238
 Asp Cys Cys Gly Tyr Cys Val Gly Ala Ile Cys Leu
 65 70 75

atggtgttt ctctctccct c 259

0110 62

0111 76

0112 PPT

4110- Conus omaria

4111- 61

Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Tyr Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu
20 25 30

Leu Ser Asn Ala His Asn Glu Met Lys Asn Pro Glu Ala Ser Thr Leu
35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Ile Leu Tyr Ser
50 55 60

Asp Cys Cys Gly Tyr Cys Val Gly Ala Ile Cys Leu
65 70 75

4112- 63

4113- 65

4114- FFT

4115- Conus omaria

4116-

4117- SITE

4118- (1)..(25)

4119- Xaa at residue m6 may be Glu or gamma-carboxy-Glu; Xaa at residues
11 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s
ulpho-Tyr or O-phospho-Tyr

4120- 67

Cys Leu Gly Phe Gly Xaa Ala Cys Leu Ile Leu Xaa Ser Asp Cys Cys
1 5 10 15

Gly Xaa Cys Val Gly Ala Ile Cys Leu
20 25

4121- 64

4122- 162

4123- DNA

4124- Conus aulicus

4125-

4126- SDS

4127- (1)..(240)

4128- 64

atg aaa atg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ctt 96
Tyr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

ttt tgg aag aca caa cac aaa atg aag aac ccc gaa gcc tct aaa ttg 144
Ile Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag aag tgc aaa gca gaa aat gaa ctt tgt aat ata ttt ata caa 192
Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln
50 55 60

aac tgg tgc gac ggg acg tgc ctt ctt atc tgc ata caa aat cca cag 240

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln
65 70 75 80

tgatatttttcttctactacc tc

262

4210 65
4211 30
4212 PFT
4213 Conus aulicus

4210 65
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln
50 55 60

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln
65 70 75 80

4210 66
4211 30
4212 PFT
4213 Conus aulicus

4210 67
4211 SITE
4212 (1)..(29)
4213 Xaa at residues 4 and 6 may be Glu or gamma-carboxy-Glu; Xaa at re
sidue 28 may be Pro or hydroxy-Pro

4210 66
Cys Lys Ala Xaa Asn Xaa Leu Cys Asn Ile Phe Ile Gln Asn Cys Cys
1 5 10 15

Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Xaa Gln
20 25

4210 67
4211 258
4212 ENA
4213 Conus aulicus

4210 68
4211 CDS
4212 (1)..(228)

4210 67
Arg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

48

Arg aaa ttt gcc acg gct gat gac ccc aga aat gga ttg gat aat cgt
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg
20 25 30

96

Arg tog aag gca cgt cac gaa atg aat aac cgc aga gcc tct aaa ttg
Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu

144

35 40 45
 aac aag agg tgc ctt gag ttt ggt gaa ctt tgt aat ttt ttt ttc cca 192
 Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro
 50 55 60
 aac tgc tgc ggc tat tgc gtt ctt ctt gtc tgc cta taaactaccg 238
 Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
 65 70 75
 taatattttt ttttccctc 258
 1110 68
 1111 70
 1112 PPT
 1113 *Conus aulicus*
 1100 69
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Thr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg
 20 25 30
 Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro
 50 55 60
 Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
 65 70 75
 1110 69
 1111 68
 1112 PPT
 1113 *Conus aulicus*
 1100
 1101 SITE
 1102 (1)..(25)
 1103 Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
 residue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
 o-Tyr
 1100 69
 Cys Leu Xaa Phe Gly Xaa Leu Cys Asn Phe Phe Phe Xaa Thr Cys Cys
 1 5 10 15
 Gly Xaa Lys Val Leu Leu Val Cys Leu
 20 25
 1110 70
 1111 203
 1112 DCA
 1113 *Conus galli*
 1100
 1101 NDS
 1102 (1)..(231)
 1100 70
 atg aaa ctg acg tgt gtg atg atc gtt got gtg ctg ttc ttg acc gcc 48

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttt gtc atg gct gat gac tcc gga aat gga ttg gaa aat ctg 96
 Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
 20 25 30
 ttt tgg aag gca cat cac gaa atg aag aac cct gaa gcc tct aaa ttg 144
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aar aag aag tgc gct caa agc agt gaa tta tgt gat gcg ctg gac tca 192
 Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser
 50 55 60
 gac tgc tgc agt ggt gtt tgc atg gta ttt ttc tgc cta taaaactgcc 241
 Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu
 65 70 75
 ctgatgtctt ctctatcccc tc 263

1100 71
 1110 77
 1120 PRT
 1130 Conus dalli

1100 71
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser
 50 55 60
 Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu
 65 70 75

1110 72
 1115 26
 1120 PRT
 1130 Conus dalli

1120
 1125 SITE
 1130 (1)..(26)
 1135 Xaa at residue 6 may be Glu or gamma-carboxy-Glu.

1100 71
 Cys Ala Gln Ser Ser Xaa Leu Cys Asp Ala Leu Asp Ser Asp Cys Cys
 1 5 10 15
 Ser Gly Val Cys Met Val Phe Phe Cys Leu
 20 25

1110 73
 1115 159
 1120 TNA
 1130 Conus distans

<210>

<211> CDS

<212> (1)..(222)

<400> 73

atg aga ctg acg tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aga ttc gtc acg gct gaa gac ccc aga gat gga ttg agg aat ctt 96
Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu
20 25 30

tta tta aat gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac gaa agg tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt tat tca 192
Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
50 55 60

gac tgc tgc aac tat tgc gtt ggt gct gtc tgc cta taaaactacc 238
Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu
65 70 75

ggatgtctt ctactcccat c 259

<210> 74

<211> 76

<212> PFT

<213> Conus distans

<400> 74

Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu
20 25 30

Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
50 55 60

Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu
65 70 75

<210> 75

<211> 85

<212> PFT

<213> Conus distans

<214>

<215> SITE

<216> (1)..(25)

<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residues
12 and 18 may be Tyr, 115-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s
ulpho-Tyr or O-phospho-Tyr

<400> 75

Cys Leu Gly Phe Gly Xaa Ala Cys Leu Met Leu Xaa Ser Asp Cys Cys
1 5 10 15

Ser Met Cys Val Gly Ala Val Cys Leu
20 25

<210> 76
<211> 764
<212> FNA
<213> Conus pennaceus

<220>
<221> CDS
<222> (1)..(231)

14000 76
129 4aa ctg acg tgc ctg atg acc gtt gct gtg ctg ttc ttg acc gcc 49
Met Lys Leu Thr Cys Leu Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
129 4aa ttt ggc acg gct gaa gac ccc aga aat gga ttg gag aat ctt 96
Tyr Thr Phe Ala Thr Ala Glu Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30
129 4aa ttt tgg aag gca cat cac gaa atg aag aac cct gaa gac tct aaa ttg 144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
35 40 45
129 4aa aag agg tgc gtt aaa tat ctt gac cct tgt gac atg tta cgc cac 192
Asp Lys Arg Cys Val Lys Tyr Leu Asp Pro Cys Asp Met Leu Arg His
50 55 60
129 4aa tgc tgc ttt ggc ctg tgc gta cta ata gcc tgc atc taaaactgcc 241
Thr Cys Cys Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
65 70 75
129 4aa atgatatctt ctactcccat c 262

<210> 77
<211> 77
<212> FPF
<213> Conus pennaceus

14000 77
129 4aa Met Lys Leu Thr Cys Leu Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
129 4aa Tyr Thr Phe Ala Thr Ala Glu Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30
129 4aa Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
35 40 45
129 4aa Asp Lys Arg Cys Val Lys Tyr Leu Asp Pro Cys Asp Met Leu Arg His
50 55 60
129 4aa Thr Cys Cys Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
65 70 75

<210> 78
<211> 26
<212> FPF
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(26)

<110> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or hydroxy-Pro

<110> 78
Cys Val Lys Xaa Leu Asp Xaa Cys Asp Met Leu Arg His Thr Cys Cys
1 5 10 15

Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
20 25

<110> 79
<111> 259
<112> DNA
<113> Conus pennaceus

<110>
<111> CDS
<112> (1)..(238)

<110> 79
atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aac ttt gcc acg gct gat gac gcc aga aat gga ttg ggg aat ctt 96
Tyr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

ttt ttg aat gaa cat cac gaa atg aag aac ccc gaa gct tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac gag agg tgc ctt ggg ttt ggt gaa gtt tgc aat ttc ttt ttt cca 192
Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro
50 55 60

aac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta taaaactacc 238
Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

gtatgtctt ctattccct c 59

<110> 80
<111> 76
<112> PRT
<113> Conus pennaceus

<110> 80
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Tyr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro
50 55 60

Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

<210> 31
 <211> 15
 <212> PPT
 <213> Genus pennaceus

<220>
 <221> SITE
 <222> (1)...(25)
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 31
 Cys Leu Gly Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Asn Cys Cys
 1 5 10 15
 Ser Xaa Cys Val Ala Leu Val Cys Leu
 20 25

<210> 42
 <211> 160
 <212> DNA
 <213> Genus pennaceus

<220>
 <221> SPS
 <222> (1)...(140)

<400> 31
 atg aaa ctg aag tgc gtg atg ctc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Leu Val Ala Val Leu Phe Leu Thr Ala 15
 1 5 10 15
 gag aca ttc gcc aag gct gat gac tcc agc aat gga ctg gag aat ctt 96
 Thr Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu 30
 20 25 30
 grr tgg aag gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 45
 35 40 45
 gag aag agg tgc att cca caa ttt gat cct tgt gac atg gta cgt cac 192
 Asn Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His 60
 50 55 60
 act tgc tgc aaa ggg ttg tgc gta cta ata gcc tgc tct aaa act gcg 240
 Thr Cys Cys Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala 80
 65 70 75 80
 tgatgtcttc atctcccttc 260

<210> 33
 <211> 30
 <212> PPT
 <213> Genus pennaceus

<400> 33
 Met Lys Leu Thr Cys Val Met Leu Val Ala Val Leu Phe Leu Thr Ala 15
 1 5 10 15
 Thr Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu 30
 10 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu

35 40 45
 Asp Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His
 25 55 60
 Thr Cys Cys Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala
 65 70 75 80

4000 84
 4011 19
 4012 FFT
 4013 Conus pennaceus

4020
 4021 SITE
 4022 (1)..(24)
 4023 Xaa at residues 3 and 7 may be Pro or hydroxy-Pro.

4000 84
 Cys Ile Xaa Gln Phe Asp Xaa Cys Asp Met Val Arg His Thr Cys Cys
 1 5 10 15
 Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala
 20 25

4010 85
 4011 160
 4012 DNA
 4013 Conus pennaceus

4020
 4021 C13
 4022 (1)..(140)

4000 85 48
 atg aaa ctg aag tgc ttg atg atc gtt gct gtg ctg ttc ttg acc gcc
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

4010 86 96
 tgg aca ttc gcc aag gct gat gac ccc aga aat gga ttg gag aat ttt
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
 20 25 30

4020 87 144
 att ttg aag aca caa cac gaa atg aag aac ccc gaa gcc tct aaa ttg
 Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

4030 88 192
 aat aag aag tgc aaa gca gaa agt gaa gct tgt aat ata att aca caa
 Asn Lys Arg Cys Lys Ala Glu Ser Glu Ala Cys Asn Ile Ile Thr Gln
 50 55 60

4040 89 240
 aat tgc tgc gac ggc aag tgc ctt ttt ttc tgc ata caa att cca gag
 Asn Cys Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu
 65 70 75 80

4050 90 260
 agagcattc tctcccatc

4060 91
 4061 80
 4062 FFT
 4063 Conus pennaceus

4000 86
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
 20 25 30
 Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Lys Ala Glu Ser Glu Ala Cys Asn Ile Ile Thr Gln
 50 55 60
 Asn Cys Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu
 65 70 75 80

1118 87

1119 89

1120 187

1121 Conus pennaceus

1122

1123 SITE

1124 (1) .. (29)

1125 Xaa at residues 4, 5 and 19 may be Glu or gamma-carboxy-Glu; Xaa
 at residue 28 may be Pro or hydroxy-Pro

1126 87

Cys Lys Ala Xaa Ser Xaa Ala Cys Asn Ile Ile Thr Gln Asn Cys Cys
 1 5 10 15

Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Xaa Xaa
 20 25

1127 83

1128 832

1129 CNA

1130 Conus omaria

1131

1132 IDS

1133 (110) .. (199)

1134 83

ggtgacatc atcatcatca tccatccatc tctccatcca tccattcatt ccttcgctgc 60
 caactgtca taaatatctg agtctctctt tctgtttgta tctgacaga ttg aac aag 118
 Leu Asn Lys
 1

aga tgc att gac ggt ggt gaa att tgt gat att ttt ttt cca aac tgc 165
 Arg Cys Ile Asp Gly Gly Glu Ile Cys Asp Ile Phe Phe Pro Asn Cys
 5 10 15

tgc agt ggg tgg tgc att att ctg gtc tgc gca tgaaactacc gtgatgtctt 219
 Cys Ser Gly Trp Cys Ile Ile Leu Val Cys Ala
 25 30

caactcctt ctagtagtag tagggggggg ctctagagga tccaagetta cgtacgctg 279

tatggagagt catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt 339

awaacatcgt gactgggaaa acctgggggt taccbaactt aatcgccttg cagcacatcc 399

ccctttcgcc agctggggtg atagagaaga ggccgcacc gatcgcctt ccaacagttt 459

ggnccatccctg aatggcggaat gggacgcgcc ctgtacgggc gcattaagcg cggcgggtgt 519
 ggagggtact cgcagcgtga cgggtacact tgcacgcgcc ctacgcgcgc ctccttttgc 579
 ttcttccctt cctttctctg ccacgcctcg ccgggggttt tcccgtaag etc 632

4100 89
 4110 30
 4120 PPT
 4130 Conus omaria

4140 89
 Leu Asn Cys Arg Cys Ile Asp Gly Gly Glu Ile Cys Asp Ile Phe Phe
 1 5 10 15
 Pro Asn Cys Cys Ser Gly Trp Cys Ile Ile Leu Val Cys Ala
 20 25 30

4100 89
 4110 26
 4120 PPT
 4130 Conus omaria

4140
 4150 SITE
 4160 (1) .. (26)
 4170 Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 14 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
 mid-Trp

4200 89
 Cys Ile Asp Gly Gly Xaa Ile Cys Asp Ile Phe Phe Xaa Asn Cys Cys
 1 5 10 15
 Ser Gly Xaa Cys Ile Ile Leu Val Cys Ala
 20 25

4100 81
 4110 650
 4120 GNA
 4130 Conus omaria

4200
 4210 SDS
 4220 (107) .. (196)

4300 91
 ggtgagatc atcatcatcg atccatctgt ccacccatcc attcattcat tgcctgccag 60
 acgtccaaa atattcgagt ctctccttct gtttgtatct gacaga ttg aac aag 115
 Leu Asn Lys
 1
 aggttac ctt gac ggt ggt gaa att tgt ggt att ttg ttt cca agc tgc 163
 Ala Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro Ser Cys
 5 10 15
 ttc att ggg tgg tgc att gtt ctg gtc tgc gca tgaaactacc gtgatgtctt 216
 Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
 20 25 30
 ctactccct ctagtagtag tagggcgccg ctctagagga tccaagctta cgtacgcgtg 276
 catgcagct catagctctt ctatagtgtc acctaaatto aattcactgg ccgtcgtttt 336

aatgcttgcg gactgggaaa accctggcgt tacccaactt aatgccttg cagcacatcc 396
 cctttrgca agctggcgta atagcgaaga ggcgcgcacc gatcgccctt cccaacaagt 456
 tttgcaactt gaatggcgaa tgggaagcgc cctgttagcgg cgcattaagc gggcggggtg 516
 tttgcttac ggcacacgtg accgctacac ttgcacgcgc cctagccgcc cgtccttttc 576
 gttttttc : cttcctttct cgcacgttcg gcgggctttc cccgtcaagc tctaaatcgg 636
 ggttttct tttt 650

<110> 91
 <111> 34
 <112> FRT
 <113> Genus emaria

<110> 92
 Leu Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe
 1 5 10 15
 Ile Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
 20 25 30

<110> 93
 <111> 37
 <112> FRT
 <113> Genus emaria

<110>
 <111> SITE
 <112> (1)..(26)
 <113> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 15 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
 mo-Trp

<110> 93
 Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys
 1 5 10 15
 Ser Gly Xaa Cys Ile Val Leu Val Cys Ala
 20 25

<110> 94
 <111> 618
 <112> FNA
 <113> Genus marmoreus

<110>
 <111> CDS
 <112> (107)..(193)

<110> 94
 atgagacatc atcatcatcg atccatctgt ccattccatcc atccattcat tgcgtgccag 60
 atgtaataa atattcgagt ctctctttct gtttgtatct gacaga tgg aac aag 115
 Leu Asn Lys
 1
 aga tgc ctt gag ttt ggt gaa gtt tgt aat ttt ttt ttc cca acc tgc 163
 Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe Pro Thr Cys
 5 10 15
 tgc ggc tat tgc gtt ctt ctt gtc tgc cta taaaactacc gtgatgtctt 213

Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
25

ctactacact ctagtactag taggcggccg ctctagagga tccaagctta cgtacgcgtg 273
ctgcacagct catagctctt ctatagtgtc acctaaattc aattcaactgg cgtcgtttt 333
ataagtcgt gactgggaaa acctggggt taccacaactt aatcgcttg cagcacatcc 393
catttcgac agctggcgta atagcgaaga ggcgcgcacc gatcgccctt cccaacagtt 453
gacagctgt aatggcgaat gggacgcgc ctgttagcggc gcattaagcg cggcgggtgt 513
ggaatttag ccagcgtga ccgtacact tgcagcgccc tagcgccgc tcctttcgt 573
ttcttcctt cctttctgc cagtttcgc ggtttcccc gtcaa 618

410 21
411 19
412 PRT
413 Conus marmoreus

440 30
Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
1 5 10 15

Pro Tyr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
20 25

410 26
411 23
412 PRT
413 Conus marmoreus

410
411 SITE
412 (1) .. (25)
413 Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
o-Tyr

440 30
Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys
1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu
20 25

410 37
411 444
412 DNA
413 Conus marmoreus

410
411 CDS
412 (150) .. (236)

440 37
gaagctgtgt aagcctgcag gtaccggtcc ggaattcccg ggtagacatc atcatcatca 60
tcgatccatc tgtcatcca tccattcaat cattegtgtc cagactgtaa taaatattcg 120
agttttctct tatgtttgta tctgacagg ttg aac aag agg tgc caa gag ttc 173

Leu Asn Lys Arg Cys Gln Glu Phe
 1 5
 ggt gaa gtt tgt aat ttt ttt ttc cca gac tgc tgc ggc tat tgc gtt 221
 Gly Glu Val Cys Asn Phe Phe Phe Pro Asp Cys Cys Gly Tyr Cys Val
 10 15 20
 ctt tta ttc tgc ata taaaactacc gtgatgtctt ctcttcccat ctagtagtag 276
 Leu Leu Leu Cys Ile
 25
 tagttagtagt aggggggggc totagaggat ccaagcttac gtacgctgc atggagcgtc 336
 atagctcttc tatagtgtca cctaaattca attcaatggc cgtcgtttta caacgctgt 396
 gactgggaaa acctggcgt tcccaactta attgcgcttg cagcacat 444
 4110 98
 4111 29
 4112 PRT
 4113 Conus marmoreus
 4140 98
 Leu Asn Lys Arg Cys Gln Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
 1 5 10 15
 Pro Asp Cys Cys Gly Tyr Cys Val Leu Leu Leu Cys Ile
 20 25
 4110 99
 4111 15
 4112 PRT
 4113 Conus marmoreus
 4119
 4121 SITE
 4122 (1)..(25)
 4123 Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
 residue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr,
 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
 -Tyr
 4180 99
 Cys Gln Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Asp Cys Cys
 1 5 10 15
 Gly Xaa Cys Val Leu Leu Leu Cys Ile
 20 25
 4110 100
 4111 545
 4112 ENA
 4113 Conus omaria
 4120
 4121 SDS
 4122 (153)..(242)
 4123
 4124 misc_feature
 4125 (1)..(545)
 4126 n may be any nucleotide
 4190 100

ttttttagen ggtagcgcctg caggtaccgg tccggaattc ccgggtcgac atcatcatca	60
tcctccatcc atctgtccat ccctccattc attcattcgc taacagactg taataaatat	120
tcctccatct cttttctgttt gtatctgaca ga ttg gac aag agg tgc att cca	173
Leu Asp Lys Arg Cys Ile Pro	
1 5	
cat ttt gac cct tgt gac ccg ata cgc cac acc tgc tgc ttt ggc ctg	221
His Phe Asp Pro Cys Asp Pro Ile Arg His Thr Cys Cys Phe Gly Leu	
10 15 16	
taa tta cta ata ggc tgc atc taaaactgcc gtgatgctt ctctccct	272
Cys Leu Leu Ile Ala Cys Ile	
17 30	
cta ttagtat tagggggcgc ctctagagga tccaagctta cgtacgcgtg catgcgcagt	332
ctatagctctt ctatagtgtc acctaaattc aattcaactgg ccgtcgtttt acaacgtcgt	392
gatttgaaa accttggcgt taccgaactt aatcgccctg cagcacatcc ccctttcgcc	452
agctggcgta atagcgaaga ggcccgccac gatcgccctt cccaacagtt ggcgcagcgt	512
atggcgaat gggacgcgcc ctgtagcgcg gct	545

101
 30
 PET
 Conus maria

101
 Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg
 5 10 15
 His Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 20 25 30

10. 102
11. 26
12. 157
13. Genus omaria

11 SITE
12 (1)..(26)
13 Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.

1400 102
 Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys
 5 10 15
 Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 20 25

110 103
 111 534
 112 RNA
 113 Genus omaria

000000 CDS
000000 (140) .. (226)

<400> 103
 ggtagctgtg caggtaacggg tccggaattc cgggggtgag atcatcatca tcatccatc 60
 tgcacacaca tccatttttt catttgctgc cagactgtaa taaatattcg agtctctctt 120
 tctgtttgta tctgacaga ttg aac aag agg tgc ctt gag ttt ggt gaa gtt 172
 Cys Asn Lys Arg Cys Leu Glu Phe Gly Glu Val
 1 5 10
 tgt aac ttt ttt ttc cca acc tgc tgc ggc tat tgc gtt ctt ctt gtc 220
 Cys Asn Phe Phe Phe Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val
 15 20 25
 ttt cta taaaactacc gtgatgtctt ctcttccctt ctagttagtag taggcggcgc 276
 Cys Leu
 ctctagagga tccaagctta cgtacggcgg catgcgaagt catagctctt ctatagtgtc 336
 acctaaatc aattcaactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt 396
 taccacatt aatgccttg cagcacatcc ccttttcgcc agctggcgta atagcgaaga 456
 ggccacacc gatgcacctt cccaacagtt ggcgcagctg aatggcgaat gggacgcgcc 516
 cgtatgggc gcattaag 534
 <400> 104
 <411> 29
 <412> PFT
 <413> Conus omaria
 <400> 104
 Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
 1 5 10 15
 Phe Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
 20 25
 <400> 105
 <411> 29
 <412> iFT
 <413> Conus omaria
 <400>
 <411> SITE
 <412> (1)..(25)
 <413> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
 esidue13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
 o-Tyr
 <400> 105
 Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys
 1 5 10 15
 Gly Xaa Cys Val Leu Leu Val Cys Leu
 20 25
 <400> 106
 <411> 280
 <412> TNA
 <413> Conus obscurus

<220>
 <221> CDS
 <222> (73)..(180)

<400> 106
 cyatccatccat gtcacatccat ccattcggttc gtccgctgcc aaactgtaat aaataaccga 60
 gtctctctgt tt gta tct gac aga tgc aaa aag caa tgc cgt caa aat ggt 111
 Val Ser Asp Arg Ser Lys Lys Gln Cys Arg Gln Asn Gly 10
 1
 gaa gtg tgt gat gcg aat ttg gca cac tgc tgc agt ggc ccg tgt ttt 159
 Gln Val Cys Asp Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe 25
 15
 ctg ttg tgt cta aac cag ccg tgatgtcttc tactccctc 200
 Leu Phe Cys Leu Asn Gln Pro 35
 20

<210> 107
 <211> 38
 <212> PBT
 <213> Genus obscurus

<400> 107
 Val Ser Asp Arg Ser Lys Lys Gln Cys Arg Gln Asn Gly Glu Val Cys 15
 1
 5
 Arg Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe Leu Phe Cys 30
 20
 25
 100 Asn Gln Pro 25

<210> 108
 <211> 32
 <212> PBT
 <213> Genus obscurus

<210>
 <211> SITE
 <222> (1)..(32)
 <223> Xaa at residue 10 may be Glu or gamma-carboxy-Glu; Xaa at residue
 s 23 and 32 may be Pro or hydroxy-Pro

<400> 108
 Ser Lys Lys Gln Cys Arg Gln Asn Gly Xaa Val Cys Asp Ala Asn Leu 15
 1
 5
 Ala His Cys Cys Ser Gly Xaa Cys Phe Leu Phe Cys Leu Asn Gln Xaa 30
 20
 25

<210> 109
 <211> 262
 <212> DNA
 <213> Genus ammiralis

<210>
 <211> CDS
 <222> (1)..(231)

<400> 109
 atg aaa ctg acg tgc gtg atg atc att gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala

1 5 10 15 96
 tgg aca ttt gcc acg gct gat gac tcc gga aat gga ttg gaa aat ctt
 Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
 20 35 30
 ttt tgg aag gca cat cac gaa atg aag aac ccc aaa gcc tct aaa ttg 144
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
 35 40 45
 aac aag agg tgc act caa agc ggt gaa ctt tgt gat gtg ata gac cca 192
 Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro
 50 55 60
 gac tgg tgg aat aat ttt tgc att ata ttt ttc tgc ata taaaactgcc 241
 Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
 65 70 75
 gtgaaggctt ctactccct c 262

<10> 110
 <11> 77
 <12> FFT
 <13> Conus ammiralis

<10> 110
 Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro
 50 55 60
 Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
 65 70 75

<10> 111
 <11> 80
 <12> FFT
 <13> Conus ammiralis

<10>
 <11> SITE
 <12> (1)..(26)
 <13> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 13 may be Pro or hydroxy-Pro

<10> 111
 Cys Thr Gln Ser Gly Xaa Leu Cys Asp Val Ile Asp Xaa Asp Cys Cys
 1 5 10 15
 Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
 20 25

<10> 112
 <11> 186
 <12> DNA
 <13> Conus textile

<2.10>
 <2.11> CDS
 <2.12> (25)..(255)

<490> 112 51
 ggcataact aaaacatcac caaa atg aaa ctg acg tgc atg atc atc gtt
 Met Lys Leu Thr Cys Met Met Ile Val
 1 5

get atg ctg ttc ttg acc gcc tgg aca ttc gcc acg gct gat gac tcc 99
 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Ser
 10 15 20 25

gga aat gga ttg gag aaa ctt ttt tgg aat gca cat cac gaa atg aag 147
 Gly Asn Gly Leu Glu Lys Leu Phe Ser Asn Ala His His Glu Met Lys
 30 35 40

aac ccc gaa gcc tct aat ttg aac aag agg tgc gct cct ttt ctt cac 195
 Asn Pro Glu Ala Ser Asn Leu Asn Lys Arg Cys Ala Pro Phe Leu His
 45 50 55

cca tgc acc ttt ttc ttc cca aac tgc tgc aac ggc tat tgc gtt caa 243
 Leu Cys Thr Phe Phe Phe Pro Asn Cys Cys Asn Gly Tyr Cys Val Gln
 60 65 70

ttt atc tgc cta taaaactact gtgatgctt ctattccct c 286
 Phe Ile Cys Leu
 75

<2.10> 113
 <2.11> 77
 <2.12> PFT
 <2.13> Conus textile

<490> 113
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Asn Leu
 35 40 45

Asn Lys Arg Cys Ala Pro Phe Leu His Leu Cys Thr Phe Phe Phe Pro
 50 55 60

Asn Cys Cys Asn Gly Tyr Cys Val Gln Phe Ile Cys Leu
 65 70 75

<2.10> 114
 <2.11> 26
 <2.12> PFT
 <2.13> Conus textile

<2.10>
 <2.11> SITE
 <2.12> (1)..(26)
 <2.13> Xaa at residues 3 and 13 may be Pro or hydroxy-Pro; Xaa at residu
 e 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-
 Tyr or O-phospho-Tyr

<490> 114
 Cys Ala Xaa Phe Leu His Leu Cys Thr Phe Phe Phe Xaa Asn Cys Cys

1 5 10 15

Asn Gly Xaa Cys Val Gln Phe Ile Cys Leu
20 25

<210> 115
<111> 484
<112> DNA
<113> Conus marmoreus

<220>
<221> CDS
<222> (74)..(394)

<230> 115
gggtccagg acagtgaatt tggcttcaca gttttccact gtctgttttg gcatcatcca 60
aaatcatcac aag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg 100
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu
1 5 10

ttt ttg acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga 157
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
15 20 25

ttg gag aat ctt ttt tgc aag gca cat cac gaa atg aag aac ccc aaa 205
Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys
30 35 40

gac tct aaa ttg aac aag agg tgc ctt gac gct ggt gaa atg tgt gat 253
Asp Ser Lys Leu Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp
45 50 55 60

ctt ttt aat tca aaa tgc tgc agt ggg tgg tgc att att ctc ttc tgc 301
Leu Phe Asn Ser Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys
65 70 75

gga taaaaactacc gtgatgtctt ctactccct ctgtgctacc tggcttgatc 354
Ala

tttgattggc gcggtgcctt cactgggttat gaacccccct gatccgactc tctggcggcc 414
tgggggttc aacatccaaa taaagccgac acgatactga cgtagaaaaa aaaaaaaaaa 474
aaaaaaaaa 484

<240> 116
<241> 77
<242> PRT
<243> Conus marmoreus

<250> 116
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp Leu Phe Asn Ser
50 55 60

Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys Ala
60 70 75

<110> 117
<111> 16
<112> PFT
<113> Conus marmoreus

<120>
<121> SITE
<122> (1)..(26)
<123> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
19 may be Trp or bromo-Trp

<400> 117
Cys Leu Asp Ala Gly Xaa Met Cys Asp Leu Phe Asn Ser Lys Cys Cys
1 5 10 15

Ser Gly Xaa Cys Ile Ile Leu Phe Cys Ala
20 25

<110> 118
<111> 437
<112> DNA
<113> Conus marmoreus

<120>
<121> CDS
<122> (19)..(249)

<400> 118
tcgaaacaca tcacaaag atg aaa ctg acg agc atg atg atc gtt gct gtg 51
Met Lys Leu Thr Ser Met Met Ile Val Ala Val
1 5 10

atg ttg ttg acc gcc tgg aca ttc gtc acg got gac gac tcc gga aat 99
Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn
15 20 25

gga ttg gag aat ctt ttt tgg aag gca cat cac gag atg aag aac ccc 147
Gly Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro
30 35 40

aaa gac tct aaa ttg aac aag agg tgc ctt gac ggt ggt gaa att tgt 195
Lys Asp Ser Lys Leu Asn Lys Arg Cys Ile Asp Gly Gly Glu Ile Cys
45 50 55

ggg att ttg ttt cca agc tgc tgc agt ggg tgg tgc att gtt ctc gtc 243
Gly Ile Leu Phe Pro Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val
60 65 70 75

tgt gca tgaactacc gtgatgtctt ctactccct ctgtgtacc tgggttgatc 299
Lys Ala

tcgattggc ggtgtccctt cactggttat gaaccccccct gatccgactc tctggcggcc 359

tgggggttc aacatccaaa taaagcgaca cgacaatgac aaaaaaaaaa aaaaaaaaaa 419

aaaaaaaa

<110> 119
<111> 77
<112> PFT

<213> Conus marmoreus

<400> 119
Met Lys Leu Thr Ser Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
20 25 30
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu
35 40 45
Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro
50 55 60
Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
65 70 75

<10> 119
<11> 26
<12> PFT
<13> Conus marmoreus

<100>
<11> SITE
<12> (1)..(26)
<13> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
mo-Trp

<400> 110
Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys
1 5 10 15
Ser Gly Xaa Cys Ile Val Leu Val Cys Ala
20 25

<100> 121
<11> 470
<12> ENA
<13> Conus marmoreus

<100>
<11> CDS
<12> (70)..(303)

<400> 121
gtagcacag tgaatttggc atcacagttt tccastgtcg tctttggcat catccaaaac 60
atcaccaag atg aaa ctg acg tgc atg atg atc gaa gca gag ctg ttc ttg 111
Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu
1 5 10
acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gag 159
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu
15 20 25 30
aat ctt ttt tgg aag gca cat cac gaa atg aag aac ccc gaa gcc tct 207
Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45
aaa ttg aac aag agg tgc ctt aac act ygr gaa tta tgt gat gtg gtt 255
Lys Leu Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val
50 55 60

gaa caa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cct ata 303
 Glu Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile
 65 70 75

taactatcgt tatgtctctct actccctctct gtgctgcctg gcttgatctt tgattggcgc 363

gtgacatcca atgggttatga accccctga ccgaactctc ttgcggcctc aggggttcaa 423

cattcaata tagcgatcgc aaaatgaaaa aaaaaaaaaa aaaaaaa 470

4210- 121

4211- 78

4212- PPT

4213- *Conus marmoreus*

4400- 122

Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu Thr Ala
 1 5 10 15

Tyr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Ala Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
 50 55 60

Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile
 65 70 75

4210- 123

4211- 17

4212- PPT

4213- *Conus marmoreus*

4210-

4211- SITE

4212- (11..127)

4213- Xaa at residues 2 and 26 may be Pro or hydroxy-Pro; Xaa at residues
 6 and 12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 a
 nd 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho
 -Tyr or O-phospho-Tyr

4400- 123

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
 1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Xaa Ile
 20 25

4210- 124

4211- 470

4212- 10A

4213- *Conus marmoreus*

4210-

4211- CDS

4212- (87)..(312)

4400- 124

ttggaagggtg aatttgcctt atattttct actgtcgtct ttggcatcat ccaaaacatc 60

atcdaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg 108

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu
 1 5 10

acc acc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta ttg 156
 Thr Ala Thr Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu
 15 20 25 30

gag att ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc 204
 Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala
 35 40 45

tat aac ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat ttt 252
 Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe
 50 55 60

tat gac ttg ttt aac att ggg ccg cct tgc tgc agt gcc tgg tgc ttc 300
 Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe
 65 70 75

cac agt tgc gcc taaaactgcc gtgatgtctt ctattccct ctgtgctacc 352
 Leu Trp Cys Ala
 80

tggttgatc tttgatiggc gcgtgccctt cagtggitat gaacccccct gatccgactc 412

tctgaggcc togggggttc aacatccaaa taagctgac aacacaataa aaaaaaaaa 470

4000 115
 4011 80
 4111 PFT
 4113 Conus marmoreus

4000 115
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn
 20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
 35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
 50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
 65 70 75 80

Cys Ala

4000 126
 4011 80
 4111 PFT
 4113 Conus marmoreus

4000
 4011 SITE
 4022 (1) (30)
 4023 Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at r
 esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue
 s 24 and 28 may be Trp or bromo-Trp

4000 126
 Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile

1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
20 25 30

<210> 127
 <211> 277
 <212> DNA
 <213> *Opuntia striatus*

<214>
 <215> CDS
 <216> (1)..(246)

<400> 127
 atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala 15
 1 5 10 15

tta aca ttc gtc acg gct gtg cct cac tcc agc gat cca ttg gag aat 96
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn 30
 20 25 30

cct tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc tct aaa 144
 Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys 45
 35 40 45

tta aac gtp aga gac gac gag tcc gaa cct cct gga gat ttt tgt gcc 192
 Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly 60
 50 55 60

tta tat aca att ggg cag cct tcc tgc agt gcc tgg tgc ttc ctc tgg 240
 Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp 80
 65 70 75 80

tac gca taaactgcc gtgatgtctt ctctccct c 277
 Cys Ala

<100> 127
 <110> 32
 <120> PFT
 <130> *Opuntia striatus*

<400> 127
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala 15
 1 5 10 15

trp thr phe val thr ala val pro his ser ser asp ala leu glu asn 30
 20 25 30

leu tyr leu lys ala leu his glu thr glu asn his glu ala ser lys 45
 35 40 45

leu asn val arg asp asp glu cys glu pro pro gly asp phe cys gly 60
 50 55 60

the phe lys ile gly pro pro cys cys ser gly trp cys phe leu trp 80
 65 70 75 80

Cys Ala

<110> 129
 <111> 30
 <212> PFT

<215> Conus striatus

<216>

<217> SITE

<218> (11)...(20)

<219> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 14 and 28 may be Trp or Bromo-Trp

<410> 129

Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
20 25 30

<217> 133

<218> 177

<219> RNA

<215> Conus omaria

<410>

<411> HIS

<412> (1)...(210)

<413> 190

arg uua cty agy tgc gtc acg atc utr gct gtg cag ttg ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

trp aca ttc gtc acc gct gtg cct cac tcc agc aat gca ttg gaa aat 96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

cct tat ctc aag gca cgt cac gaa atg gaa aac ccc gaa gcc tct aaa 144
Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

ttg aac acc aga gac gac gat tgc gaa cct cct gga aat ttt tgt gcc 192
Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
50 55 60

atg ata aaa att ggg ccc cct ttc tcc agt ggc tgg tcc ttt ttc gcc 240
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80

tgc gcc taataactgcc gtgatgtctt ctcctccct c 277
Cys Ala

<410> 191

<411> 32

<412> PFT

<413> Conus omaria

<410> 131

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
 15 55 60

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
 65 70 75 80

Cys Ala

<110> 181
 <111> 30
 <112> PRT
 <113> Conus omaria

<114>
 <115> SITE
 <116> (1)..(30)
 <117> Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues
 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may
 be Trp or bromo-Trp

<118> 122
 Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
 1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
 20 25 30

<119> 133
 <1110> 177
 <1111> DNA
 <1112> Conus aulicus

<1113>
 <1114> CDS
 <1115> (1)..(246)

<1116> 135
 att aaa ctg acg tgc ctg atg ata gtt gct gtg ctg ttc ttg acc gcc 18
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gca ttg gag aat 36
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
 20 25 30

cct tat ctg aag gca cgt cac gaa atg gaa aac ccc gaa gcc tct aaa 144
 Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
 35 40 45

aaa aat acg aga gac tac gat tgc gaa cct cct gga aat ttt tgt ggc 192
 Met Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
 50 55 60

aaa aaa aat ggg cag cct tgc tgc agt ggc tgg tgc ttt ttc gcc 240
 Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
 65 70 75 80

aaa gcc taaaactgcc gtgatgtctt ctctccct c 277
 Tyr Ala

<1116> 134
 <1117> 32
 <1118> PRT
 <1119> Conus aulicus

<400> 134
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30
Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
3 40 45
Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
50 55 60
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80
Cys Ala

0110 135
0111 30
0112 PFT
0113 Conus aulicus

<400>
0121 SITE
0122 (1..30)
0123 Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 may be Glu or
gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or
hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

<400> 135
Arg Xaa Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
1 5 10 15
Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
20 25 30

0113 136
0114 345
0115 IMA
0116 Conus marmoreus

0117
0118 CDS
0119 (111)..(212)

<400> 136
ggagacatc atcattatca tccatccatc tctccatcca tctattcatt ccttcgtggc 60
cactctgtaa taaataatgc aagtcctctc tctctgttgt atctgacaga ttg aac 116
Leu Asn
1
acc aga gac gac gat tgc gaa cct cct gga aat ttt tgt ggc atg ata 164
Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly Met Ile
5 10 15
aac att ggg ccg cct tgc tgc agt ggc tgg tcc ttt ttc gcc tgc gcc 212
Lys Ile Gly Pro Pro Cys Ser Gly Trp Cys Phe Phe Ala Cys Ala
20 25 30
ttaaactgcc gtgatgtctt ctcttccct ctagtagtag taggcggccg ctctagagga 272

tccaagctta cgtacgcgtg catgcgacgt catagctctt ctatagtgtc acctaaattc 332
 aattcaactgg ccgtcgtttt acaacgttcgt gactgggaaa accctggcgt taccocaaatt 392
 aatcgccttg cagcacatcc ccttttcgac agctggcgta atagcgaaga ggccgcaccc 452
 gatcgccttg ccccaacatt ggcagcctg aatggcgaat gggacgcgac ctgtacgcgc 512
 gcatcgcgt cggcggttct ggtggttacg ccgcgcgcgt gacccgtac acttgccagc 572
 gactacgc cgcctctttt cgtttcttct cctctttctt cgcacgttc gccgctttt 632
 cgcgcacgc tctaaatcgg ggcctctttt agggcgcgat ttaagtgcct tac 685

<210> 137
 <211> 34
 <212> PBT
 <213> *Conus marmoreus*

<400> 137
 Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
 1 5 10 15
 Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
 20 25 30

Cys Ala

<100> 137
 <110> 30
 <112> PBT
 <113> *Conus marmoreus*

<210>
 <211> WITE
 <212> (1)... (30)
 <213> Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues
 6, 7, 11 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may
 be Trp or bromo-Trp

<400> 137
 Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
 1 5 10 15
 Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
 20 25 30

<100> 139
 <110> 126
 <112> DNA
 <113> *Conus regius*

<210>
 <211> CDS
 <212> (1)... (94)

<400> 139
 ttaaac cag aga gac tgc ctt agt aaa aac gct ttc tgt gcc tgg ccg 48
 Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro
 1 5 10 15
 ata ctt gga caa ctg tgc tgc agt ggc tgg tgc tta tac gtc tgc atg 96
 Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
 20 25 30

taaaactgac gtgatgtctt ctatcccttc

<21> 141
 <21> 32
 <21> PPT
 <21> *Canus regius*

<40> 140
 Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro
 1 5 10 15
 Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
 20 25 30

<11> 141
 <11> 28
 <11> PPT
 <11> *Canus regius*

<11> SITE
 <11> (11...128)
 <11> Xaa at residues 11 and 21 may be Trp or bromo-Trp; Xaa at residue
 12 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be T
 yr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
 pho-Tyr

<40> 141
 Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa
 1 5 10 15
 Leu Cys Cys Ser Gly Xaa Cys Leu Xaa Val Cys Met
 20 25

<11> 140
 <11> 132
 <11> DNA
 <11> *Canus radiatus*

<11>
 <11> GDS
 <11> (11...103)

<40> 141
 a t g a a g a a g a a g g t g a t g a c t g c t t g c t t a a a a a a a t t g t g g c
 1 5 10 15
 Leu Asn Lys Lys Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly

t t t c c a a a t t t g g a g g g c c a t g c t g c a g t g g c t t g t g c t t t t t c g t c
 10 15 30
 Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val

t t t g c c t a a a a c t g c c g t g a t g t c t t c t a c c c c c t
 Cys Ala

<11> 143
 <11> 34
 <11> PPT
 <11> *Canus radiatus*

<40> 143
 Leu Asn Lys Lys Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly
 1 5 10 15

Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val
 20 25 30

Cys Ala

<11> 144
 <11> 20
 <11> PPT
 <11> Conus radiatus

<11>
 <11> SITE
 <11> (1)..
 <11> Xaa at residues 14 and 19 may be Pro or hydroxy-Pro.

<11> 144
 Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly Phe Xaa Lys Leu
 1 5 10 15

Gly Gly Xaa Cys Cys Ser Gly Leu Cys Phe Phe Val Cys Ala
 20 25 30

<11> 145
 <11> 127
 <11> LNA
 <11> Conus regius

<11>
 <11> GDS
 <11> (1)..
 <11> 146

ttg aat cag agc gac tgc ctt cct aga gac aca ttc tgt gcc ttg ccg 48
 Leu Asn Gln Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro
 1 5 10 15

gaa ctt gga cta ctg tgc tgc agt ggc cgg tgc tta ctc ttc tgc gtg 96
 Gln Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
 10 25 30

*aaagtgc gtagtgtctt ctctccct c 127

<11> 146
 <11> 31
 <11> PPT
 <11> Conus regius

<11> 146
 Leu Asn Gln Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro
 1 5 10 15

Gln Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
 20 25 30

<11> 147
 <11> 31
 <11> PPT
 <11> Conus regius

<11>
 <11> SITE
 <11> (1)..
 <11> Xaa at residues 4 and 12 may be Pro or hydroxy-Pro.

<400> 147
 Asp Cys Leu Xaa Arg Asp Thr Phe Cys Ala Leu Xaa Gln Leu Gly Leu
 1 5 10 15

Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
 20 25

<210> 148
 <211> 345
 <212> 1NA
 <213> Genus aurisiacus

<214>
 <215> 1BS
 <216> 11... (234)

<400> 148
 atg aaa ctg acg tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tga aca ttc gtc acg gct gat gac acc aga aat gga ctg aag aat ctt 96
 Thr Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30

ttt ttc aag gca cgt cat gaa atg aag aac acc gaa gcc tct aaa ttg 144
 Phe Phe Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

aat aag aga cat ggg tgc tct aat gct ggt gca ttt tct ggc atc cat 192
 Asn Lys Arg Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
 50 55 60

gaa gga ttc tgc tgc agc gag att tgc att gtt tgg tgc aca 234
 Pro Gly Leu Cys Cys Ser Glu Ile Cys Ile Val Trp Cys Thr
 65 70 75

tgagtcgcat tctgctggta catcttgctggt ctccaacgga ggactctgct gcagcaacct 284

tgtttatctt ttctgtgctgct thaatattt gtgatgtctt ctactccat c 345

<210> 149
 <211> 78
 <212> 1BT
 <213> Genus aurisiacus

<400> 149
 Met Cys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30

Phe Phe Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Ile Cys Ile Val Trp Cys Thr
 65 70 75

<210> 150
 <211> 27

<212> PRT
 <213> *Pinus aurisiacus*

<220>
 <221> FITE
 <222> (1)...(27)

<223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or brom-Trp

<400> 150
 Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Ile Cys Ile Val Xaa Cys Thr
 20 25

<410> 151
 <411> 412
 <412> DNA
 <413> *Conus purpurascens*

<420>
 <421> CTS
 <422> (1)...(243)

<430> 171
 aag aag atg aag tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aat ttc gtc aag gct gat gac tcc aaa aat gga ctg gag aat cat 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgt gaa gcc tct aaa ttg 144
 Ile Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 35 40 45

gac aag aag gaa gcc tgc tat gcg cct ggt act ttt tgt ggc ata aag 192
 Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60

acc ggc cta tgc tgc agt gag ttt tgt ctc ccg ggc gtc tgc ttc ggt 240
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
 65 70 75 80

ggt aaactgacct gatgttctct actccctctt gtgtacctg gcttgatctt 293
 Gly

tgtatggcgt gtgccttcca ctggttatga accactgat cttacctctc ttgaaggacc 353

tgtggggtcc agcatccaaa taagcgacat cccaatgaaa aaaaaaaaaa aaaaaaaaaa 412

<440> 152
 <441> 81
 <442> PRT
 <443> *Conus purpurascens*

<450> 152
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Tyr Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

Pro Tyr Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

His Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
65 70 75 80

Gly

<110> 153

<111> 29

<112> PPT

<113> *Conus purpurascens*

<114>

<115> SITE

<116> (11...29)

<117> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<118> 154

Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

<119> 154

<120> 29

<121> PPT

<122> *Conus purpurascens*

<123>

<124> SITE

<125> (11...29)

<126> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<127> 154

Xaa Ala Cys Xaa Ala Xaa Gly Thr Ala Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

<128> 155

<129> 29

<130> PPT

<131> *Conus purpurascens*

<132>

<133> SITE

<134> (11...29)

<135> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
or hydroxy-Pro

<400> 156
Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ala Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
2 25

<100> 156
<110> 22
<120> FFT
<130> Genus purpurascens

<400>
<110> SIE
<120> (11..19)
<130> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
or hydroxy-Pro

<400> 156
Xaa Ala Cys Xaa Ala Xaa Gly Ala Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

<100> 157
<110> 289
<120> DNA
<130> Genus magus

<400>
<110> CTS
<120> (11..232)

<400> 157
atg aag atg aag tgc gtg atg atc gtt gct gtg ctg ttc ttg acc acc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

tgt aca ttc gtc aag gct gat gac tcc aga tat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

ttt aag aag gca cgt tat gaa atg aag aac cct gaa jcc tct aaa ttg 144
Phe Phe Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

ttt aag aca gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt 192
Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
50 55 60

tta gaa ctc tgc tgc agc gag ttt tgc ttt tta tgg tcc ata aca ttt 240
Phe Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

gtt gat ttt ggc taacagtgtg cgttggttag tgtcttctcc tccctcc 289
Val Asp Ser Gly

<400> 158

<211> 84
 <212> PRT
 <213> Conus magus

<400> 150
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
 50 55 60
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80
 Val Asp Ser Gly

<110> 150
 <111> 30
 <112> PRT
 <113> Conus magus

<114>
 <115> SITE
 <116> 11... (32)
 <117> Xaa at residue 4 may be Tyr, 1:5-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
 hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
 Xaa at residue 25 may be Trp or bromo-Trp

<400> 150
 Asp Gly Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu
 1 5 10 15
 Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser
 20 25 30

<210> 160
 <211> 200
 <212> tNA
 <213> Conus magus

<214>
 <215> GTS
 <216> 11... (249)

<400> 160
 atg aag ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc acc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr 15
 1 5 10
 tgg aca ttc atc acg gct gat gac tcc aga tat gga ttg aag aat att 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu 30
 10
 ttt ccg aag aca cgt cat gaa atg aag aac cct gaa gac tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 45
 35 40

aac aag aga gat gaa tgc tat cct cct ggt aca ttt tgt ggc atc aaa 192
 Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 55 60
 cca aca ctt tgc tgc agc gag ata tgc tta tgg ttt gtc tgc ata tca 240
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80
 ttt tat ttt tgaattgatgt cttctctctcc cctc 273
 Phe Asp Phe

<210> 161
 <211> 82
 <212> PFI
 <213> Citrus magus

<300> 161
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 Thr Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 Phe Phe Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 Phe Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80
 Phe Asp Phe

<100> 161
 <110> 82
 <112> PFI
 <113> Citrus magus

<210>
 <211> SITE
 <212> (1)... 32)
 <213> Xaa at residue 2 may be Glu or gamma-carboxy-Glu; Xaa at residue
 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr; Xaa at residues 5, 6 and 14 may be Pro or hydro
 xy-Pro

<400> 161
 Asp Xaa Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15
 Tyr Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe
 20 25 30

<110> 163
 <112> 149
 <113> SBA
 <114> Citrus magus

<210>
 <211> IDS
 <212> (1)... (252)

<400> 163
 atg aaa ctg aag tgc gtg atg atc gtt gct gta ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc aag gct gat gac tcc aga tat gga ctg aag gat ctg 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
 20 25 30
 ttc ccg aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac cag aga gaa ccc tgc tat aat gct ggt tca ttt tct ggc atc cat 192
 Asn Glu Arg Glu Ala Cys Tyr Asn Ala Gly Ser Phe Cys Gly Ile His
 50 55 60
 cca gaa ctg tgc tgc aag gag ttt tgc att ctt tag ttc ata aca ttt 240
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Ile Leu Trp Cys Ile Thr Phe
 65 70 75 80
 gtt gat tct ggc taactgtgtg cgttggttga tctctctctc tcccatc 289
 Val Asp Ser Gly

<10> 164
 <10> 34
 <10> PFT
 <10> Genus magus

<400> 164
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
 20 25 30
 Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Glu Arg Glu Ala Cys Tyr Asn Ala Gly Ser Phe Cys Gly Ile His
 50 55 60
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Ile Leu Trp Cys Ile Thr Phe
 65 70 75 80
 Val Asp Ser Gly

<100> 165
 <100> 32
 <100> PFT
 <100> Genus magus

<200>
 <200> SITE
 <200> 1) (32)
 <200> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr; Xaa at residue 11 may be Pro or hydrox
 y-Pro; Xaa at residue 25 may be Trp or bromo-Trp

<400> 165
 Xaa Ala Cys Xaa Asn Ala Gly Ser Phe Cys Gly Ile His Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Ile Leu Xaa Cys Ile Thr Phe Val Asp Ser
 20 25 30

<210> 166
 <211> 171
 <212> 1NA
 <213> Conus magus

<214>
 <215> MS
 <216> (11...249)

<400> 166
 atg aag ctg acg tgc atg atg atc gtt gct gta ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tac aca ttc gtc acg gct gat gac tcc aga tat gga ctg aag gat ctg 96
 Tyr Ile Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
 20 25 30

tac aca aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Phe Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

atc aca aia gaa gcc tgc tat aat ggt ggt aca ttt tgt ggc atc aaa 192
 Asn Ser Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys
 50 55 60

cca gga ctt tgc tgc agc gag ata tgc tta tcc ttt gtc tgc ata tca 240
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80

tat gat ttg attgagtct tctctctccc tc 271
 Phe Asp Leu

<160> 167
 <161> 98
 <162> PBT
 <163> Conus magus

<400> 167
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Tyr Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
 20 25 30

Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Ser Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys
 50 55 60

Ile Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80

Ile Asp Leu

<210> 168
 <211> 98
 <212> PBT
 <213> Conus magus

<210>

<211> SITE

<212> (1)...(22)

<213> Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro

<400> 168

Xaa Ala Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe
20 25 30

<210> 169

<211> 271

<212> DNA

<213> Canus ermineus

<400>

<401> CDS

<402> (1)...(243)

<403> 169

atg aag ctg aag tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc aag gct gat gac tcc aaa aat gga ctg gag aat cat 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

tgt tgg aag gca cgt gac gaa atg aag aac ggc gaa gcc tct aaa ttg 144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

aac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

atg ggc cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240
Met Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65 70 75 80

agt taactacggt gatgtttctt cctccctc 272
Arg

<210> 170

<211> 21

<212> PPT

<213> Canus ermineus

<400> 170

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

Pro Gly Ieu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
6 70 75 80

Gly

<111> 171
<112> 25
<113> PFT
<114> Conus ermineus

<115>
<116> SITE
<117> (1)..(20)
<118> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
lpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be
Pro or hydroxy-Pro

<411> 172
Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
20 25

<119> 173
<1110> 173
<1111> 1NA
<1112> Conus purpurascens

<1113>
<1114> CDS
<1115> (1)..(143)

<1116> 172
atg aag atg acg tgc atg atg atc gtt gct gtg ctg ttc ttg act gcc 43
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgc aca ttc ttc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
Tyr Phe Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
10 25 30

tta tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
Ile Thr Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

gac aac aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

acc ggt ata tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65 70 75 80

att taactgcagt gatgtcttct cctccctc 272
Arg

<1117> 173
<1118> 81
<1119> PFT
<1120> Conus purpurascens

<1121> 173

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Tip Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30
 Phe Tip Lys Ala Arg Asp Glu Met Lys Arg Arg Glu Ala Ser Lys Leu
 35 40 45
 Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 Phe Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
 65 70 75 80

Gly

1160- 174
 1110- 24
 1110- PBT
 1110- Conus purpurascens

1120- 1120
 1120- SITE
 1120- (1) (230)
 1120- Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr; Xaa at residues 14 and 24 may be Pro o
 r hydroxy-Pro

1130- 174
 Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15
 Lys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
 20 25

1140- 175
 1110- 166
 1110- RNA
 1110- Conus striatus

1150- 175
 1110- CDS
 1110- (1) (240)

1160- 175
 atg aag ctg aag tgc gtc atg atc gtt gct gtc ctg ttc ttg acc act 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 tgg acc ttc ttc aag gct gat gac tcc aga tat gga ttg aag aat ctt 96
 Tip Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 ttt ccc aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 His Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 ttt aat aga gaa ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cat 192
 Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
 50 55 60
 cca gja ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240

266

A. 175
 A. 82
 A. PBT
 A. *Conus striatus*

Trp Trp Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
16 25 30

Pro Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
36 40 45

Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
54 55 60

Phe Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 (7.) 75 80

12. App

177
91
957
Genus striatus

```

100
101 SITE
102 (11..21)
103 Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
104 residue 14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tr
105 p or bromo-Trp

```

499-177
Xaa Gly Cys Ser Ser Gly Gly Thr ILe Cys Gly Ile His Xaa Gly Leu
5 10 15

Tyr Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Trp Phe Ile Asp
 20 25 30

10	173
11	166
12	ENA
13	Conus striatus

11-11-68
11-11-68
11-11-68

188
 gaa gaa gta acg tgc gtg atg atc gtt gct gtg cgc ttc ttg acc act
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 5 10 15

48

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu

96

20 25 30
 ttt cgt aag gga cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Phe Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aat aat aat gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cat 192
 Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
 50 55 60
 cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240
 Phe Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80
 atr gat tgatgtcttc tctctcctc 266
 Ile Asp
 119- 179
 111- 82
 111- PFT
 113- *Conus striatus*
 119- 179
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 Phe Ile Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
 50 55 60
 Phe Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80
 Ile Asp
 119- 180
 111- 21
 111- PFT
 113- *Conus striatus*
 120-
 121- SITE
 122- (1)...(31)
 123- Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue
 14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or br
 omo-Trp
 120- 180
 Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His Xaa Gly Leu
 1 5 10 15
 Cys Lys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
 20 25 30
 119- 191
 111- 21
 111- PFT
 121- *Conus striolatus*

<211>

<211> SITE

<212> (1)..(21)

<213> Xaa at residues 6 and 14 may be Pro or hydroxy-Pro; Xaa at residue 1 may be Glu or gamma-carboxy-Glu

<411> 181

Ser	Lys	Cys	Phe	Ser	Xaa	Gly	Thr	Phe	Cys	Gly	Ile	Lys	Xaa	Gly	Leu
1				5					10					15	

Cys	Cys	Ser	Val	Arg	Cys	Phe	Ser	Leu	Phe	Cys	Ile	Ser	Phe	Xaa
			20					25					30	

<412> 182

<412> 245

<412> DNA

<413> Conus catus

<414>

<414> SDS

<414> (1)..(244)

<415> 182

Met	Lys	Leu	Thr	Cys	Met	Met	Ile	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala
1				5				10					15		

Trp	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Lys	Asn	Leu
			20					25				30			

Phe	Pro	Lys	Ala	Arg	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Leu
		35					40					45			

Asn	Lys	Arg	Tyr	Gly	Cys	Ser	Asn	Ala	Gly	Ala	Phe	Cys	Gly	Ile	His
	50					55					60				

Pro	Gly	Leu	Cys	Cys	Ser	Glu	Leu	Cys	Leu	Val	Trp	Cys	Thr
			70					75					

gagtgatatt	tatttttgta	catttttggtg	attcaacgga	ggaacttgct	gcagcaacct

gagtgatatt	tatttttgta	catttttggtg	attcaacgga	ggaacttgct	gcagcaacct

<416> 183

<416> 78

<416> PFT

<416> Conus catus

<417> 183

Met	Lys	Leu	Thr	Cys	Met	Met	Ile	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala
1				5				10					15		

Trp	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Lys	Asn	Leu
			20					25				30			

Pro	Lys	Ala	Arg	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Leu
		35				40					45			

Asn	Lys	Arg	Tyr	Gly	Cys	Ser	Asn	Ala	Gly	Ala	Phe	Cys	Gly	Ile	His
	50					55					60				

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr
6 70 75

1100 184
1110 27
1120 PRT
1130 Conus catus

1140
1150 SITE
1160 (1)..(27)
1170 Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
pyrroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
Xaa at residue 25 may be Trp or bromo-Trp

1180 184
Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Val Xaa Cys Thr
20 25

1200 185
1210 345
1220 PMA
1230 Conus catus

1240
1250 CES
1260 (1)..(234)

1270 185
1280 aag atg atg atg atg gtt gct gtg ctg ttc ttg acc gcc 48
1290 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
1300 ttc aca ttc gtc acg gct gat gac tcc aga tat gga ctg aag aat ctt 96
1310 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
10 25 30
1320 ttt aag aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
1330 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45
1340 aac aag aga tat ggg tgc tct aat gct ggt gca ttt tct ggc atc cat 192
1350 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
50 55 60
1360 aca gga ctc tgc tgc agc gag ctt tgc ctg ggt tgg tgc aca 234
1370 Phe Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr
65 70 75
1380 tgggtgctat tctactgcta catcttggtggt cttcaacgga ggactctgct gcagcaacct 294
1390 tgggttatct tctgtgtggtt aacatttggt gatgtctctt ctattccct c 345

1400 186
1410 78
1420 PRT
1430 Conus catus

1440 186
1450 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala

48	ctg	aaa	ctg	acg	tgt	ctg	atg	atc	gtt	gct	gtg	cag	ttc	ttg	acc	gcc	
	Met	Lys	Leu	Thr	Cys	Leu	Met	Ile	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala	
					5				10						15		
96	tgg	aca	ttc	gtc	acg	gct	gat	gac	tcc	aga	aat	gga	ttg	gag	aat	ctc	
	Cys	Thr	Ile	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Glu	Asn	Leu	
				20					25					30			
144	tct	cag	aag	gca	cct	cac	gaa	atg	aag	aac	ccc	gaa	gcc	tct	aaa	tcg	
	Ser	Phe	Lys	Ala	Pro	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Ser	
			35					40					45				
192	aac	aac	aga	tat	gag	tgc	tat	cta	cag	tta	cat	ttt	tgt	ggc	atc	aac	
	Asn	Lys	Arg	Tyr	Glu	Cys	Tyr	Leu	Leu	Val	His	Phe	Cys	Gly	Ile	Asn	
			50				55					60					
240	gca	gga	ctc	tgc	tgc	agg	aac	ctt	cgc	tta	ttt	ttc	gtg	tgc	tta	aca	
	Gly	Gly	Leu	Cys	Cys	Ser	Asn	Leu	Cys	Leu	Phe	Phe	Val	Cys	Leu	Thr	
						70					75					80	

ttt tgg tgatgttctt tcttccctc
Phe Ser

<110> 189
<111> 32
<112> PFT
<113> Conus distans

<400> 189
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Thr Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30
Ser Pro Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45
Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn
50 55 60
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Ile Ser

<110> 190
<111> 31
<112> PFT
<113> Conus distans

<400> 190
<110> SITE
<111> (1)..(31)
<112> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 190
Xaa Xaa Cys Xaa Leu Leu Val His Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15
Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

<110> 191
<111> 113
<112> INA
<113> Conus regius

<400> 191
<110> CDS
<111> (1)..(93)

<400> 191
tgg agc aag aga gac tgc ctt cct gac tac acg att tgt gcc ttc aat
1 5 10 15
Leu Ser Lys Arg Asp Cys Leu Pro Asp Tyr Thr Ile Cys Ala Phe Asn
20 25 30
atg agt ctg tgc tgc agc gac aag tgc atg ctc gtc tgc ctg ccg
Met Gly Leu Cys Cys Ser Asp Lys Cys Met Leu Val Cys Leu Pro
25 30

tgatgttctt tcttccctc

48

93

113

<110> 192
 <111> 31
 <112> PRT
 <113> *Canus regius*

<114> 192
 Leu Ser Cys Arg Asp Cys Leu Pro Asp Tyr Thr Ile Cys Ala Phe Asn
 1 5 10 15
 Met Gly Leu Cys Cys Ser Asp Lys Cys Met Leu Val Cys Leu Pro
 20 25 30

<115> 193
 <116> 17
 <117> PRT
 <118> *Canus regius*

<119>
 <120> 511E
 <121> (1)...(37)
 <122> Xaa at residues 5 and 27 may be Pro or hydroxy-Pro; Xaa at residu
 e 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T
 yrosine or O-phospho-Tyr

<123> 194
 Asp Cys Leu Xaa Asp Xaa Thr Ile Cys Ala Phe Asn Met Gly Leu Cys
 1 5 10 15
 Cys Ser Asp Lys Cys Met Leu Val Cys Leu Xaa
 20 25

<124> 194
 <125> 116
 <126> PRT
 <127> *Canus regius*

<128>
 <129> CDS
 <130> (1)...(96)

<131> 194
 tta aat aag aga atc atc tgc ttt cct gac tac atg ttt tgt ggc gtc 48
 Leu Asn Lys Arg Ile Ile Cys Phe Pro Asp Tyr Met Phe Cys Gly Val
 1 5 10 15
 aat gtg ttt cgg tgc tgc agt ggc aac tgc ctt ctc atc tgc gtg cgg 96
 Asn Val Phe Leu Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Pro
 20 25 30
 taaatctctc tactccctc 116

<132> 195
 <133> 37
 <134> PRT
 <135> *Canus regius*

<136> 195
 Leu Asn Lys Arg Ile Ile Cys Phe Pro Asp Tyr Met Phe Cys Gly Val
 1 5 10 15
 Asn Val Phe Leu Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Pro
 20 25 30

<137> 196

<211> 19
 <211> PFT
 <211> Conus regius

<220>
 <221> SITE
 <221> (1)...(28)
 <223> Xaa at residues 5 and 28 may be Pro or hydroxy-Pro; Xaa at residue
 ... 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 196
 119 Ile Cys Gly Xaa Asp Xaa Met Phe Cys Gly Val Asn Val Phe Leu
 1 5 10 15
 Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Xaa
 20 25

<210> 197
 <211> 259
 <212> DNA
 <213> Conus gloriamaris

<220>
 <221> CDS
 <222> (1)...(238)

<400> 197
 119 aag aag atg aag tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 120 Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 121 aca ttc ttc aag gct gtg cct cac tcc agc aat gcg ttg gag aat 96
 122 Thr Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
 20 25 30
 123 tat tat atg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa 144
 124 Tyr Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 35 40 45
 125 aac aag agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac 192
 126 Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
 50 55 60
 127 tgc tgc aat ggc tgg tgc att ttc gcc tgc ctc taaaactgtc 238
 128 Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu
 65 70 75
 129 atgatgatt ctctctccct c 259

<210> 198
 <211> 76
 <212> PFT
 <213> Conus gloriamaris

<400> 198
 147 Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 148 Thr Thr Thr Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
 20 25 30
 149 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu
 65 70 75

228- 199
 229- 24
 230- PFT
 231- *Conus gloriamaris*

232-
 233- SITE
 234- (1) .. (24)
 235- Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or primo-Trp

400- 199
 Tyr Xaa Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser
 1 5 10 15

Gly Xaa Cys Ile Phe Ala Cys Leu
 20

236- 199
 237- 258
 238- INA
 239- *Conus dalli*

240-
 241- PFS
 242- (1) .. (218)

440- 199
 Arg aaa atg acg tgc att atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Ile Met Ile Val Ala Val Leu Phe Leu Thr Ala 15

441- 199
 Arg aca ttc gtc acg gct gtg cct cac tcc agc aat gcg ttg gag aat 96
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn 30

442- 199
 ctt tat atg aag gca cat cat gaa atg aac aac ccc gag gac tct gaa 144
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu 45

443- 199
 tta aat aag agg tgc tat cat ggt ggg aca ggt tgt gac tct gga aac 192
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn 60

444- 199
 tta ttt tgc agt agc tgg tgc att ttc gtc tgc ctc taaaactgcc 238
 Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Cys Leu 75

445- 199
 tta ttt tgc agt agc tgg tgc att ttc gtc tgc ctc taaaactgcc 258

446- 199
 447- 26
 448- PFT
 449- *Conus dalli*

450- 201
 Met Lys Leu Thr Cys Ile Met Ile Val Ala Val Leu Phe Leu Thr Ala

1				5					10						15
Trp	Thr	Phe	Val	Thr	Ala	Val	Pro	His	Ser	Ser	Asn	Ala	Leu	Glu	Asn
			20					25					30		
Leu	Tyr	Ileu	Lys	Ala	His	His	Glu	Met	Asn	Asn	Pro	Glu	Asp	Ser	Glu
		5					40					45			
Ileu	Asn	Lys	Arg	Cys	Tyr	Asp	Gly	Gly	Thr	Gly	Cys	Asp	Ser	Gly	Asn
	50					55					60				
Gln	Cys	Cys	Ser	Gly	Trp	Cys	Ile	Phe	Val	Cys	Leu				
65					70					75					

10) 12

12 34

11 1953

1. Dennis Halli

100

SITE

222 (1) .. (24)

212 (1) (184)
213 Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
n, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
pyrro-Trp

1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 26

100-101
 Cys Met Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser
 5 10 15

Gly Met Cys Ile Phe Val Cys Leu

254 200

211 - 219

210 296A

115 *Canis pennaceus*

100

103

1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544, 1545, 1546, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1555, 1556, 1557, 1558, 1559, 1560, 1561, 1562, 1563, 1564, 1565, 1566, 1567, 1568, 1569, 1570, 1571, 1572, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1584, 1585, 1586, 1587, 1588, 1589, 1590, 1591, 1592, 1593, 1594, 1595, 1596, 1597, 1598, 1599, 1600, 1601, 1602, 1603, 1604, 1605, 1606, 1607, 1608, 1609, 1610, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1621, 1622, 1623, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1631, 1632, 1633, 1634, 1635, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644, 1645, 1646, 1647, 1648, 1649, 1650, 1651, 1652, 1653, 1654, 1655, 1656, 1657, 1658, 1659, 1660, 1661, 1662, 1663, 1664, 1665, 1666, 1667, 1668, 1669, 1670, 1671, 1672, 1673, 1674, 1675, 1676, 1677, 1678, 1679, 1680, 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1699, 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709, 1710, 1711, 1712, 1713, 1714, 1715, 1716, 1717, 1718, 1719, 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1733, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752, 1753, 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770, 1771, 1772, 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788, 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806, 1807, 1808, 1809, 1810, 1811, 1812, 1813, 1814, 1815, 1816, 1817, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848, 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1857, 1858, 1859, 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871, 1872, 1873, 1874, 1875, 1876, 1877, 1878, 1879, 1880, 1881, 1882, 1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898, 1899, 1900, 1901, 1902, 1903, 19

405 203

Inf - 263
 AAG aaG cGG acc tCG gTg arg atc gtt gct gTg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 5 10 15

tgg acg gtc gtc acg gct gtg cct cac tcc aac aag cgg ttg qcg aat
 Trp Thr Val Val Thr Ala Val Pro His Ser Asn Lys Arg Leu Ala Asn

20 25 30

att tat atg aag gca cgt cac gaa atg aaa aac ccc gaa gcc tct aat
 Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn

atg gat aag aag tgc ttt gag agt tgg gta gct tgt gag tct cca aaa 192
Val. Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys
50 55 60

504 tgc tgc aat cac gtg tgc att ttc gtc tgc acc tgaaactgac
 Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr
 60 70 75

gtgatgtttt ttctctccct c 259

<210> 204
 <211> 76
 <212> PPT
 <213> Conus pennaceus

<400> 204
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Val Val Thr Ala Val Pro His Ser Asn Lys Arg Leu Ala Asn
 20 25 30
 Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn
 35 40 45
 Val Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys
 50 55 60
 Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr
 65 70 75

<210> 205
 <211> 84
 <212> PPT
 <213> Conus pennaceus

<210>
 <211> SITE
 <222> (1)..(24)
 <223> Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at r
 esidue 5 may be Trp or bromo-Trp; Xaa at residue 11 may be Pro o
 r hydroxy-Pro

<400> 205
 Cys Phe Xaa Ser Xaa Val Ala Cys Xaa Ser Xaa Lys Arg Cys Cys Ser
 1 5 10 15
 His Val Cys Leu Phe Val Cys Thr
 20

<210> 206
 <211> 253
 <212> DNA
 <213> Conus distans

<210>
 <211> CDS
 <222> (1)..(228)

<400> 206
 atg aag ctg acg tgt atg ttg atc atc gct gtg ctg ttc ctg acg gcc 48
 Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgt caa ctg tct aca aat gcg agt tac gcc aga agt aag cag aag cat 96
 Lys Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His
 20 25 30
 gct gtt ctg agg tcg act gac aaa aac tcc aag ttg acc cag cgt tgc 144
 Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys
 35 40 45
 atg aag gct caa gaa cat tgc act caa aat cct gac tgc tgc agt gag 192
 Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu

50 55 60

tct tgc aat aag ttt gtc ggc aga tgc ttg tca gac tgatctgatg 238
 Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
 65 70 75

tatctctcttccatc 253

4400 207
 4410 76
 4420 PPT
 4430 Conus distans

4400 207
 Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His
 20 25 30
 Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys
 35 40 45
 Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu
 50 55 60
 Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
 65 70 75

4410 208
 4420 29
 4430 PPT
 4440 Conus distans

4400
 4410 SITE
 4420 (1)..
 4430 Xaa at residues 3, 6 and 17 may be Glu or gamma-carboxy-Glu; Xaa
 at residue 12 may be Pro or hydroxy-Pro

4400 208
 Cys Asn Xaa Ala Gln Xaa His Cys Thr Gln Asn Xaa Asp Cys Cys Ser
 1 5 10 15
 Xaa Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
 20 25

4410 209
 4420 159
 4430 BNA
 4440 Conus ammiralis

4400
 4410 CDS
 4420 (1)..
 4430 209
 ttc aac ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Ser Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gtg ccc gac tcc agc aat gcg ttg gag aat 96
 Trp Thr Phe Val Thr Ala Val Pro Asp Ser Ser Asn Ala Leu Glu Asn
 20 25 30

ctt tat ctg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa 144
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 3' 40 45

ttg aac aag agg tgc tat gat ggt gga aca agt tgt aac act gga aac 192
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn
 55 60

caa tgc tgc agt ggc tgg tgc att ttc ctc tgc ctc taaaactgcc 238
 Gln Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu
 65 70 75

atgatatctt cctctccct c 259

1210- 210
 1211- 76
 1212- PFT
 1213- *Conus ammiralis*

1400- 216
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro Asp Ser Ser Asn Ala Leu Glu Asn
 20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn
 50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu
 65 70 75

1210- 111
 1211- 14
 1212- PFT
 1213- *Conus ammiralis*

1220-
 1221- SITE
 1222- (1)..(24)
 1223- Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
 bromo-Trp

1400- 211
 Cys Xaa Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
 1 5 10 15

Gly Xaa Cys Ile Phe Leu Cys Leu
 20

1210- 212
 1211- 186
 1212- ENA
 1213- *Conus textile*

1210-
 1211- SDS
 1212- (25)..(255)

1400- 212

ggcattacct aaaacatcac caag atg aaa ctg acg tgc atg atc gtt 51
Met Lys Leu Thr Cys Met Met Ile Val
1 5

gct ggg ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gcg cct cac 99
Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Ala Pro His
10 15 20 25

tcc aac aat gcg tgg gag aat ctt tat ctg aag gca cat cat gaa atg 147
Ser Ser Asn Ala Leu Glu Asn Leu Tyr Leu Lys Ala His His Glu Met
30 35 40

aac aac ccc gaa gcc tct gaa ttg aac aag agg tgc tat gat agt ggg 195
Asn Asn Pro Glu Ala Ser Glu Leu Asn Lys Arg Cys Tyr Asp Ser Gly
45 50 55

aca agt tgt aac act gga aac caa tgc tgc agt gcc tgg tgc att ttc 243
Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp Cys Ile Phe
60 65 70

gtc tct tgc ctg taaaactacc gtagatgttt ctctccct c 286
Val Ser Cys Leu
75

01100 213
01110 27
01120 EFT
01130 Conus textile

04000 213
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Ala Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Ala Ser Glu
35 40 45

Leu Asn Lys Arg Cys Tyr Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn
50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Ser Cys Leu
65 70 75

01100 214
01110 35
01120 EFT
01130 Conus textile

02000
02010 SITE
02020 (1)...(25)
02030 Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
bromo-Trp

04000 214
Cys Xaa Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
1 5 10 15

Gly Xaa Cys Ile Phe Val Ser Cys Leu
20 25

<210> 215
 <211> 272
 <212> DNA
 <213> Conus gloriamaris

<210>
 <211> CDS
 <212> (1)..(252)

<400> 215
 atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ctg aca gcc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat ctt 96
 Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
 20 25 30
 ttt tcc aaa tca cgt gac gaa atg gag gac ccc gaa gct tct aaa ttg 144
 Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
 35 40 45
 cgg aat agg gat tgc caa gca cta tgg gat tat tgt cca gta cgg ctg 192
 Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu
 50 55 60
 ttc tca tgg ggt gat tgc tgc tat ggc tta atc tgt ggc cct ttc gtc 240
 Leu Ser Ser Gly Asp Cys Cys Tyr Gly Leu Ile Cys Gly Pro Phe Val
 65 70 75 80
 tgg att gga tgg tgaatgtottc taatccatc 272
 Cys Ile Gly Trp

<210> 216
 <211> 84
 <212> PFT
 <213> Conus gloriamaris

<400> 216
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
 20 25 30
 Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
 35 40 45
 Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu
 50 55 60
 Leu Ser Ser Gly Asp Cys Cys Tyr Gly Leu Ile Cys Gly Pro Phe Val
 65 70 75 80
 Cys Ile Gly Trp

<210> 217
 <211> 33
 <212> PFT
 <213> Conus gloriamaris

<210>
 <211> SITE
 <212> (1)..(33)

<117> Xaa at residues 6 and 33 may be Trp or bromo-Trp; Xaa at residues 8 and 31 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 27 may be Phe or hydroxy-Pro

<117> 117
 Asp Cys Gln Ala Leu Xaa Asp Xaa Cys Xaa Val Xaa Leu Leu Ser Ser
 1 5 10 15
 Gly Asp Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Ile Gly
 20 25 30

Xaa

<110> 218
 <111> 275
 <112> DNA
 <113> Conus omaria

<110>
 <111> CDS
 <112> (1)..(249)

<400> 213
 arg aad ctg aag tgg ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 taa aca ttc gtc atg gct gat gac tcc aac aat gga ctg gca aat ctt 96
 Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
 20 25 30
 ttc tgg aaa tca cgt gac gaa atg gag gat acc gat cct tct aaa ttg 144
 Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Thr Asp Pro Ser Lys Leu
 35 40 45
 gag aac aga aaa act tgc caa aga agg tgg gat ttt tgt cca gga tgg 192
 Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser
 50 55 60
 atc gtt gga gtc ata act tgc tgc ggt ggc tta atc tgt ttt ctg ttc 240
 Leu Val Gly Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe
 65 70 75 80
 ttc tgc gtt tgatagtgat gctctttctcc tccct 275
 Phe Cys Val

<110> 219
 <111> 83
 <112> FRT
 <113> Conus omaria

<400> 219
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
 20 25 30
 Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Thr Asp Pro Ser Lys Leu
 35 40 45
 Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser
 50 55 60

Leu Val Gly Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe
60 70 75 80

Ile Cys Val

01100 118

01100 119

01100 PBT

01100 *Conus omaria*

01100

01100 SITE

01100 (1) .. (32)

01100 Xaa at residue 7 may be Trp or bromo-Trp; Xaa at residue 10 may be
+ Pro or hydroxy-Pro

04000 110

Lys Thr Cys Gln Arg Arg Xaa Asp Phe Cys Xaa Gly Ser Leu Val Gly
1 5 10 15

Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe Phe Cys Val
20 25 30

01100 111

01100 112

01100 PMA

01100 *Conus dalli*

01100

01100 GDS

01100 (1) .. (246)

04000 221

atg aag atg atg atg atg atg gtt gct gtg ctg ttc ctg aca gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgc atg ata gtc atg gct gat gac tcc aac aat gga ctg ggc aat ctt 96
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

ttt tgg aaa tta cgt gac gaa atg gag gac ccc gaa ggt tct aaa ttg 144
Phe Ser Lys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu
35 40 45

tat aaa aag gat tgc caa gaa aaa tgg gat tat tgt cca gta ccg ttc 192
Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe
50 55 60

att gga tag agg tat tgc tgc gat ggc ttt atc tgt cca tct ttc ttc 240
Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe
65 70 75 80

tgc gct agatagtgat gtattctctc ttcacctc 274
Cys Ala

01100 112

01100 PBT

01100 PBT

01100 *Conus dalli*

04000 222

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

Pro Ser Cys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu
35 40 45

Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe
50 55 60

Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe
65 70 75 80

Cys Ala

110 113

111 11

112 FFT

113 Conus galli

1200

121 SITE

122 (1)..(31)

123 Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residues 8 and 13 may be Tyr, 1, 25-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 26 may be Pro or hydroxy-Pro

1400 113

Asp Cys Gln Xaa Lys Xaa Asp Xaa Cys Xaa Val Xaa Phe Leu Gly Ser
1 5 10 15

Arg Xaa Cys Cys Asp Gly Phe Ile Cys Xaa Ser Phe Phe Cys Ala
20 25 30

110 124

111 171

112 DRA

113 Conus galli

1200

121 CDS

122 (1)..(252)

1400 124

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ttg ttc ctg aca gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat cat 96
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His
20 25 30

tct tgg aaa tca cgt gac gaa atg gag gac cct gaa gct tct aaa ttg 144
Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
35 40 45

gag aaa agg gat tgc caa gcc gaa tgg gag ttt tgt ata gta ccg gtc 192
Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val
50 55 60

att gga ttt gtg tat tgc tgc ccc tgg ctt atc tgt ggc cct ttc gtc 240
Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
65 70 75 80

tgc gtt tat atc tgatgtcttc tateccctc
Cys Val Asp Ile

1118 235
1119 84
1120 FFT
1121 Genus dalli

1400 235
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His
20 25 30

Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
35 40 45

Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val
50 55 60

Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
65 70 75 80

Cys Val Asp Ile

1118 236
1119 84
1120 FFT
1121 Genus dalli

1122 SITE
1123 (1)..(33)
1124 Xaa at residues 5 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r
esidues 6 and 22 may be Trp or bromo-Trp; Xaa at residues 12, 21
and 27 may be Pro or hydroxy-Pro;

1220 SITE
1221 (1)..(33)
1222 Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-T
yr, O-sulpho-Tyr or O-phospho-Tyr

1400 236
Asp Cys Gln Gly Xaa Xaa Xaa Phe Cys Ile Val Xaa Val Leu Gly Phe
1 5 10 15

Val Xaa Cys Cys Xaa Xaa Leu Ile Cys Gly Xaa Phe Val Cys Val Asp
20 25 30

Ile

1110 217
1111 265
1112 DNA
1113 Genus pennaceus

1114
1115 GDS
1116 (1)..(234)

1400 237
atg aaa ctg acg tgc ctg atg atc att gct gtg ctg ttc ttg acc gcc

Met Lys Leu Thr Cys Leu Met Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc qts atg ggt gat gac ccc aga gat jaa ccg gag gca cgt 96
 Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg
 20 25 30
 qac gaa atg aac ccc gca gcc tct aaa ttg aac gag aga ggc tgc ctt 144
 Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
 35 40 45
 aaa ggt gat gat ttt tgc ggc ata ccg ttt gtg aac aac ggg cta tgc 192
 Glu Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys
 50 55 60
 tgc agt agc aat tgt gtt ttt gts tgc aca ccc caa ggg aag 234
 Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
 65 70 75
 taaaaatgat gtagatgttt ctcttcccat c 265

0100- 223
 0111- 78
 0112- FFT
 0113- *Conus pennaceus*

0400- 108
 Met Lys Leu Thr Cys Leu Met Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg thr phe val met ala asp asp pro arg asp glu pro glu ala arg
 20 25 30
 asp glu met asn pro ala ala ser lys leu asn glu arg gly cys leu
 35 40 45
 glu val asp tyr phe cys gly ile pro phe val asn asn gly leu cys
 50 55 60
 cys ser gly asn cys val phe val cys thr pro gln gly lys
 65 70 75

0110- 129
 0111- 81
 0112- FFT
 0113- *Conus pennaceus*

0120-
 0121- SITE
 0122- (1)..(31)
 0123- Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue
 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydrox
 y-Iro

0400- 119
 Gly Cys Leu Xaa Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn
 1 5 10 15
 Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
 20 25 30

0110- 130
 0111- 828

0210 DNA
0211 Conus marmoreus

0220
0221 CDS
0222 (122)..(229)

0400 230
gtgagacatc atcatcatcg atccatctgt ccacacatct gtccacacat ccattcattc 60
attcaactgac aaactgtcat aaatatttga gtctctcttt ctgtttttat ctgacagatt 120
t aac gag aga gac tgc ctt aat gtt gat tat ttt tgc ggc ata cag ttt 169
Asn Gln Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe
1 5 10 15
ttt aac aac ggg cta tgc tgc agt ggc aat tgt gtt ttt gtc tgc aca 217
Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr
20 25 30
ttt aac ggg aag taaaactgac gtgatgtctt ctcttccctt ctagttagtag 269
Phe Gln Gly Lys
35
tggggggggg ctctagagga tccaagotta cgtacgggtg catgcgacgt catagctctt 329
ctatagtgtc acctaaattc aattcaactgg cagtcagttt tacaacgtcg tgactgggaa 389
tacctggggg ttacctaaact taatgcgctt gcagcacat 428

0210 231
0211 36
0212 PFI
0213 Conus marmoreus

0400 231
Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe
1 5 10 15
Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr
20 25 30
Phe Gln Gly Lys
35

0210 232
0211 38
0212 PFT
0213 Conus marmoreus

0220
0221 SITE
0222 (1)..(30)
0223 Xaa at residue 6 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 11 and 29 may be Pro or hydroxy-Pro

0400 232
Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn Gly
1 5 10 15
Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
20 25 30

0108 233
 0111 217
 0112 EHA
 0113 Conus marmoreus

0208
 0211 CTS
 0212 (105) .. (224)

0408 234
 tggatattat catcatgat ccattgtgac atccatcat tcattcattc gctgccaaac 60
 tttataaat atttgagtct ctctttctgt ttttatctga caga ttg gac aag aga 116
 Leu Asp Lys Arg
 1
 ggg tgc atg gaa gct gat tat tat tgc gtc tta ccg ttt gtg ggc aac 164
 Glu Cys Leu Glu Ala Asp Tyr Tyr Cys Val Leu Pro Phe Val Gly Asn
 10 15 20
 ggg atg tgc tgc agt ggc att tgt gtt ttt gtc tgc ata gcc caa cgc 212
 Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg
 25 30 35
 ttt gaa acc gtc tga 227
 Phe Cys Thr Val
 40

0110 234
 0111 40
 0112 FFT
 0113 Conus marmoreus

0408 234
 lau asp lys arg glu cys leu glu ala asp tyr tyr cys val leu pro
 1 5 10 15
 phe val gly asn gly met cys cys ser gly ile cys val phe val cys
 20 25 30
 ile ala gln arg phe lys thr val
 35 40

0110 235
 0111 36
 0112 FFT
 0113 Conus marmoreus

0208
 0211 SITE
 0212 (11) .. (36)
 0213 Xaa at residues 1 and 4 may be Glu or gamma-carboxy-Glu; Xaa at r
 esidues 7 and 8 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr
 , O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 12 may be Pro or
 hydroxy-Pro

0408 231
 Xaa Cys Leu Xaa Ala Asp Xaa Xaa Cys Val Leu Xaa Phe Val Gly Asn
 1 5 10 15
 Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg
 20 25 30
 Phe Lys Thr Val

35
 <210> 236
 <211> 525
 <212> DNA
 <213> *Cinus marmoreus*

<214>
 <215> PDS
 <216> (131)..(241)

<40> 236
 gaaagggtgg ggaattcccg ggtcgacatc atcatcatcg atccatctgt ccacccatcc 60
 atccattatc tcattcgctg ccaaaactgtc ataaacattt gactctctct ttctgttttt 120
 atccgacaga ttg aac gag aga gac tgc ctt gaa cct gat tat gtt tgc 169
 Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys
 1 5 10
 ggc ata cgg ttt gtg ttc aac ggg cta tgc tgc agt gga att tgt gtt 217
 Gly Ile Pro Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val
 15 20 25
 ttt atc tgc ata gcc caa aag tat taaaagcgg tcatgtcttc taticccatc 271
 Phe Ile Tyr Ile Ala Gln Lys Tyr
 30 35
 tagtagtagt aggggggggc totagaggat ccaagcttac gtacggctgc atggcgacgc 331
 atagctcttc tatagtgtca cctaaattca attcaactgga cgtcgtttta caacgtcgtg 391
 atgggaataa cccggggcgtt acccaactta atcgcttgc agcacatccc cctttcgcca 451
 atgggggtaa tagccgaaga ggcgcgcacc gatcgccctt cccaacagtt ggcgcagcctg 511
 atgggggaat ggggg 525

<210> 237
 <211> 37
 <212> PFT
 <213> *Cinus marmoreus*

<400> 237
 Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys Gly Ile Pro
 1 5 10 15
 Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val Phe Ile Cys
 20 25 30
 Ile Ala Gln Lys Tyr
 35

<210> 238
 <211> 33
 <212> PFT
 <213> *Cinus marmoreus*

<214>
 <215> SITE
 <216> (1)..(33)
 <225> Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residues
 5 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 33 may
 be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O

-phospho-Tyr

<400> 23:
 Asp Cys Leu Xaa Xaa Asp Xaa Val Cys Gly Ile Xaa Phe Val Phe Asn
 1 5 10 15

Gly Leu Cys Cys Ser Gly Ile Cys Val Phe Ile Cys Ile Ala Gln Lys
 20 25 30

Xaa

210: 139
 211: 137
 212: DNA
 213: Genus marmoreus

210:
 211: 153
 212: (146)..(247)

<400> 139
 gtaagcctg caggtaccgg tcgggaattc cggggtcgac atcatcatca tcatcgatcc 60
 atctgtccat ccctctattc attcattcgc tgcbaaactg taatacatat tagaatctct 120
 cctctctttt gtatctgaca gattg gag aaa agg gcg tgc agc aaa aaa tgg 172
 Glu Lys Arg Ala Cys Ser Lys Lys Trp
 1 5

gaa tat tgt ata gta ccg atc ctt gga ttc gta tat tgc tgc cct ggc 220
 Glu Tyr Cys Ile Val Pro Ile Leu Gly Phe Val Tyr Cys Cys Pro Gly
 1 15 20 25

ttt atc tgt ggt cct ttc gtc tgc gtt tgatagtcat gtcttctcct 267
 Leu Ile Cys Gly Pro Phe Val Cys Val
 30

ccatctcagt agtagtaggc ggccgctcta gaggatccaa gcttaagtag gcgtgcacgc 327
 gtagtcacag ctctctctata gtgtcaccta aattcaattc actggcgctc gttttacaac 387
 ctgtgactg ggaaaaacct ggcggtaccc aacttaatcg ccttgcaagca catccccctt 447
 cggccggtg gggtaataag cgaagaggcc cgcaccgacg gcccttcacca acagttgcgc 507
 aacctgaatg gcgaaatggg accgcacctg 537

210: 140
 211: 134
 212: EFT
 213: Genus marmoreus

<400> 140
 Glu Lys Arg Ala Cys Ser Lys Lys Trp Glu Tyr Cys Ile Val Pro Ile
 1 5 10 15
 Val Gly Phe Val Tyr Cys Cys Pro Gly Leu Ile Cys Gly Pro Phe Val
 20 25 30

Cys Val

210: 141
 211: 131
 212: PRT

<713> Conus marmoreus

<720>

<721> SITE

<722> (1)..(31)

<723> Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residues 8 and 18 may be Tyr, 1 25-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12, 21 and 27 may be Pro or hydroxy-Pro

<740> 241

Ala Cys Ser Lys Lys Xaa Xaa Xaa Cys Ile Val Xaa Ile Leu Gly Phe
1 5 10 15

Val Xaa Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Val
20 25 30

<710> 240

<711> 241

<712> 242

<713> Conus omaria

<720>

<721> CDS

<722> (149)..(271)

<740> 242

aaagcgggta cgcctgcagg taacgggtcgg gaattccggg gtgcacatca tcatcatcat 60

tcattcatct gtccatccat ccattccattc attcaactgac aaactgtcat aaatatttga 110

gattctcttt ctgtttttat ctgcacaga ttg aac gag aga gac tgc ctt aat 172
Leu Asn Glu Arg Asp Cys Leu Asn
1 5

gac gat tat ttt tgt ggc ata ccg ttt gtg aac aac ggg cta tgc tgc 220
Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys Cys
10 15 20

gat ggc aat tgt gtt ttt tgt ctg cac acc cca agg gaa gta aaa ctg 268
Ser Gly Asn Cys Val Phe Cys Leu His Thr Pro Arg Glu Val Lys Leu
25 30 35 40

gag agatgtcttc tcttcccttc tagtagtagt aggcggcggc tctagaggat 321
Pro

aaagcttac gtacgggtgc atgcgacgtc atagctcttc tatagtgtca cctaaattca 381

attacttgc cgtcgtttta caacgtcgtg actgggaaaa ccttggcgtt acccaactta 441

agagcttac agcactccc cctttcgcca gctggcgtaa tagcgaagag gcccgcacgg 501

atggccttc ccaacagttg ccgagcctga atggagaatg ggacggccc t 552

<710> 243

<711> 241

<712> 242

<713> Conus omaria

<740> 243

Leu Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro
1 5 10 15

Phe Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu
20 25 30

His Thr Pro Arg Glu Val Lys Leu Pro
35 40

02100 244
02110 77
02120 PFT
02130 Conus omaria

02200
02210 SITE
02220 (1) .. (37)
02230 Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12, 31 and 37 may be Pro or hydroxy-Pro; Xaa at residue 33 may be Glu or gamma-carboxy-Glu

03000 244
Asp Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn
1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu His Thr Xaa Arg
20 25 30

Xaa Val Lys Leu Xaa
35

02100 245
02110 217
02120 FMA
02130 Conus obscurus

02200
02210 CDS
02220 (36) .. (181)

04000 245
ggatccatct ggcacccat ccattccatc attcattgac aaactgtaac aaatattcaa 60

gctctctt ctgtttgtgt ctgac aga tgg aaa cgg tgc ctt gtt tac ggt 110
Arg Ser Lys Arg Cys Leu Val Tyr Gly
1 5

aaa cct tgt gac tgg ctg acc att gag ggt atg gag tgc tgc agt aaa 160
Thr Pro Cys Asp Trp Leu Thr Ile Ala Gly Met Glu Cys Cys Ser Lys
10 15 20 25

atg tgc ttc atg atg tgc tgg taaaactgac gtgatgtctt ctactccct c 210
Lys Cys Phe Met Met Cys Trp
30

02100 246
02110 77
02120 PFT
02130 Conus obscurus

04000 246
Arg Ser Lys Arg Cys Leu Val Tyr Gly Thr Pro Cys Asp Trp Leu Thr
1 5 10 15

Ile Ala Gly Met Glu Cys Cys Ser Lys Lys Cys Phe Met Met Cys Trp
20 25 30

4108 247
 4111 28
 4112 PPT
 4113 Conus obscurus

4114
 4115 SITE
 4116 (1)..(28)
 4117 Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or hydroxy-Pro; Xaa at residues 10 and 28 may be Trp or bromo-Trp; Xaa at residue 17 may be Glu or gamma-carboxy-Glu

4118 247
 Cys Leu Val Xaa Gly Thr Xaa Cys Asp Xaa Leu Thr Ile Ala Gly Met
 1 5 10 15
 Xaa Cys Cys Ser Lys Lys Cys Phe Met Met Cys Xaa
 20 25

4119 248
 4111 134
 4112 BHA
 4113 Conus radiatus

4114
 4115 CFC
 4116 (1)..(109)

4117 248
 1 120 aac bag aga gac tgc cat gaa gtt ggt gaa ttt tgt ggc tta ccg 49
 Leu Asn Gln Arg Asp Cys His Glu Val Gly Glu Phe Cys Gly Leu Pro
 1 5 10 15

210 ata aag aac ggg cta tgc tgc agt cag att tgt tta ggt gtc tgc 97
 Leu Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys
 20 25 30

310 aaa atg ttt taaaaactgcc gtgatgtott ctactcccat 139
 Ala Lys Val Phe
 35

4118 249
 4111 28
 4112 PPT
 4113 Conus radiatus

4114 249
 1 120 Asn Gln Arg Asp Cys His Glu Val Gly Glu Phe Cys Gly Leu Pro
 1 5 10 15

Leu Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys
 20 25 30

Ala Lys Val Phe
 35

4119 250
 4111 28
 4112 PPT
 4113 Conus radiatus

4114
 4115 SITE

01000 101..(22)

01000 Xaa at residues 4 and 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Pro or hydroxy-Pro

01000 155

Asp Cys His Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn
1 5 10 15

Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys Ala Lys Val Phe
20 25 30

01000 151

01000 152

01000 153

01000 Conus radiatus

01000 154

01000 155

01000 156..(100)

04000 151

ata gag aag aaa gag tgc act ggc aat ggt gaa ttt tgt ggc ata tcg 49
Leu Asp Lys Lys Glu Cys Thr Ala Asn Gly Glu Phe Cys Gly Ile Ser
1 5 10 15

atc ttt aga aac tac cta tgc tgc agt ggc cgg tgt gta ttc gtc tgc 97
Val Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys
20 25 30

atc tagtgaact ggcgtgatgt cttctatccc ctt 133
Ile

01000 152

01000 153

01000 154

01000 Conus radiatus

04000 152

Leu Asp Cys Lys Glu Cys Thr Ala Asn Gly Glu Phe Cys Gly Ile Ser
1 5 10 15

Val Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys
20 25 30

Ile

01000 153

01000 154

01000 155

01000 Conus radiatus

01000 156

01000 SITE

01000 101..(29)

01000 Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

04000 153

Leu Cys Thr Ala Asn Gly Xaa Phe Cys Gly Ile Ser Val Phe Gly Ser
1 5 10 15

Xaa Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys Ile
20 25

8. 100
 9. 100
 10. 100

254
 a tta gag aag aaa gag tgc act acc aat ggt gaa ttt tgt ggc ata tgc 49
 Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser
 : 5 10 15

gta ttt taa agc ttc cta tgc tgc agt ggc ctg tgt gta ttc gtc tgc 97
Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys
20 23 30

and tagetgaact gccgtgatgt cttctcttcc cct
133

110	106
111	53
112	547
113	Cnus radiatus

10000 251
1 Met Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser
5 10 15

Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys
20 25 30

15

010 : 150
 011 : 0
 012 : PST
 013 : Conus radiatus

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100 SITE
101 (1)..(29)
102 Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu.

```

14000-136
 Ala Cys Thr Thr Asn Gly Xaa Phe Cys Gly Ile Ser Val Phe Ala Ser
 1 5 10 15
 Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys Ile
 20 25

010 157
011 153
012 14A
013 Genus radiatus

... ..
... ..
... .. (100)

400 257
 ttg gac aaq aga aaa tgc ttt ccc aaa aat cat ttt tgt ggc ttt gtg 49
 Leu Asp Lys Arg Lys Cys Phe Pro Lys Asn His Phe Cys Gly Phe Val

1 5 10 15 97

gtg atg ctg aac tac cta tgc tgc agt ggc cgg tgt ata ttc gtc tgc
 Val Met Leu Asn Tyr Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys
 20 25 30

gac ttttgaact ggcgtgatgt cttctactcc cat 133
 Val

4100 254
 4111 34
 4112 PPT
 4113 Conus radiatus

4400 214
 Leu Asp Lys Arg Lys Cys Phe Pro Lys Asn His Phe Cys Gly Phe Val
 1 5 10 15

Val Met Leu Asn Tyr Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys
 20 25 30

Val

4110 159
 4111 29
 4112 PPT
 4113 Conus radiatus

4200
 4211 SITE
 4212 (1)...(29)
 4213 Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 17 may
 be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, C-sulpho-Tyr or O
 -phospho-Tyr

4400 209
 Lys Cys Phe Xaa Lys Asn His Phe Cys Gly Phe Val Val Met Leu Asn
 1 5 10 15

Xaa Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys Val
 20 25

4110 100
 4111 130
 4112 DNA
 4113 Conus regius

4200
 4211 PDS
 4212 (1)...(99)

4400 160 48

ctg aat aag aga agc tgc ctt cct cta gac tgg ttt tgt ggc ttc aat
 Leu Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Asn
 1 5 10 15

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 Ile Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys
 20 25 30

atc taactgac gtgatgttt cttctccct c 130
 Met

4100 261

100-1
Ile Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Asn
5 10 15

12. - 13.

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141 Lys Leu Xaa Leu Asp Xaa Phe Cys Gly Phe Asn Ile Ile Gly Ala
1 5 10 15

110 163
 111 319
 112 DUA
 113 Genus delessertii

4.17. 263

96
 101 543 510 480 450 420 390 360 330 300 270 240 210 180 150 120 90 60 30
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 103 20 30

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 ... Lys Arg Asp Cys Ile Pro Gly Gly Glu Asn Cys Asp Val Phe Arg
 70 75 80

... ttc cgg tgc tgc agt gga tat tgc ata cta ctc ctt tgc gca
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85

90

95

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319

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 35 40 45
 Arg Ile Gln Thr Arg Leu Met Val Gly Gln Ser Ala Ser Lys Arg Pro
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 Ser Lys Arg Asp Cys Ile Pro Gly Gly Glu Asn Cys Asp Val Phe Arg
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 85 90 95

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<100>
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 <113> Xaa at residues 4 and 14 may be Pro or hydroxy-Pro; Xaa at residue
 7 may be Glu or gamma-carboxy-Glu; Xaa at residues 15 and 21 ma
 y be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
 O-phospho-Tyr

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 Cys Cys Ser Gly Xaa Cys Ile Leu Leu Leu Cys Ala
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<110> 206
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 ctctctttct gtttgtgtct aacaga ttg aga tgg tgc att cct agt ggt gaa 103
 Leu Arg Trp Cys Ile Pro Ser Gly Glu
 1 5
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 Leu Cys Phe Arg Ser Asp His Ile Gly Cys Cys Ser Gly Lys Cys Ala
 10 15 20 25
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 Phe Val Cys Leu
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 ttaaaaaaaa tttttt 1009

210 167

211 169

212 PBT

213 Conus striatus

240 167

Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys Phe Arg Ser Asp His
 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
 20 25

210 208

211 210

212 PBT

213 Conus striatus

210

211 SITE

212 (1) .. (29)

213 Xaa at residue3 may be Trp or bromo-Trp; Xaa at residue 6 may be
 Pro or hydroxy-Pro; Xaa at residue 9 may be Glu or gamma-carboxy
 -Glu

4400- 268
 Leu Arg Xaa Cys Ile Xaa Ser Gly Xaa Leu Cys Phe Arg Ser Asp His
 1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
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4410- 269
 4411- 270
 4412- BHA
 4413- Conus striatus

4420-
 4421- CTS
 4422- (1)..< (27)

4430- 269
 Ala Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His 48
 1 5 10 15

Ala Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His 90
 1 5 10 15

4440- 270
 4441- 271
 4442- BPT
 4443- Conus striatus

4450- 270
 Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His
 1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
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4460- 271
 4461- 272
 4462- BPT
 4463- Conus striatus

4470-
 4471- SITE
 4472- (1)..< (27)
 4473- Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be
 Pro or hydroxy-Pro

4480- 271
 Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Arg Ser Asp His Ile Gly
 1 5 10 15

Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
 20 25

4490- 272
 4491- 273
 4492- BHA
 4493- Conus striatus

4500-
 4501- CDS
 4502- (1)..< (87)

14098 172
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 14929 998
 14930 999
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 14932 1001
 14933 1002
 14934 1003
 14935 1004
 14936 1005
 14937 1006
 14938 1007
 14939 1008
 14940 1009
 14941 1010
 14942 1011
 14943 1012
 14944 1013
 14945 1014
 14946 1015
 14947 1016
 14948 1017
 14949 1018
 14950 1019
 14951 1020
 14952 1021
 14953 1022
 14954 1023
 14955 1024

4011 - 33
 4012 - PBT
 4013 - *Conus obscurus*

4014 - 276
 Val Ser Asp Arg Leu Arg Trp Cys Val Pro Ser Gly Glu Val Cys Arg
 1 5 10 15
 Arg Tyr Glu Phe Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys
 20 25 30

Ser

4010 - 217
 4011 - 22
 4012 - PBT
 4013 - *Conus obscurus*

4014 -
 4015 - SITE
 4016 - (1)..(29)
 4017 - Xaa at residue 3 may be Trp or bromo-Trp; Xaa at residue 6 may be
 Pro or hydroxy-Pro; Xaa at residues 9 and 15 may be Glu or gamma
 -carboxy-Glu; Xaa at residue 14 may be Tyr, 125-I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

4018 - 277
 Leu Arg Xaa Cys Val Xaa Ser Gly Xaa Val Cys Arg Arg Xaa Xaa Phe
 1 5 10 15
 Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys Ser
 20 25

4010 - 172
 4011 - 159
 4012 - PDA
 4013 - *Conus radiatus*

4014 -
 4015 - CDS
 4016 - (12)..(117)

4018 - 173
 atctctctct ctctgctgga c agg tgg act cgg tgc ttg cct gac gga acg 51
 Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr
 1 5 10
 tct agc ctt ttt agt agg atc aga tgc tgc ggt act tgc agt tca atc 99
 Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile
 15 20 25
 tta aag tca tgt gtg agc tgatcgggcy gttgatcttc ctccctctgt 147
 Leu Lys Ser Cys Val Ser
 30
 ctctctctct tttctgcttg agtctctctt acctgagagt ggctcatgaac cactcatcac 207
 ctctctctct ggaggcttca gaggagctac attgaaataa aagccgcatt gc 259

4010 - 179
 4011 - 22
 4012 - PBT
 4013 - *Conus radiatus*

<400> 279

Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg
 1 5 10 15

Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
 20 25 30

<400> 280

<401> 28

<402> PPT

<403> Conus radiatus

<400>

<401> SITE

<402> (1)...(28)

<403> Xaa at residue 3 may be Pro or hydroxy-Pro.

<400> 288

Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
 1 5 10 15

Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
 20 25

<400> 291

<401> 47

<402> DNA

<403> Conus geographus

<400>

<401> 250

<402> (13)...(313)

<400> 281

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aacatcacaa ag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 111
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe
 1 5 10

tgg acc gcc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta 159
 Leu Thr Ala Thr Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val
 15 20 25

tgg gag aat ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa 207
 Leu Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu
 30 35 40 45

gcc tct aaa tgg aac gtg aga gac gac gag tgc gaa cct cct gga gat 255
 Ala Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp
 50 55 60

ttt tgt agc ttt ttt aaa att ggg cgg cct tgc tgc agt ggc tgg tgc 303
 Phe Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys
 65 70 75

tta ctc tgg tgc gcc taaaaactgcc gtgatgtctt ctattccctt ctgtgtctacc 358
 Phe Leu Trp Cys Ala
 80

tggtctgata ttgtattggc gcttgccctt cagtgggttat gaacccctt gagccgactc 418

tctgggggac togggggttc aacatccaaa taaagcgaca acacaatcac aagtaaaaaa 473

<210> 282
 <211> 82
 <212> PPT
 <213> Conus geographus

<400> 282
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn
 20 25 30
 Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
 35 40 45
 Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
 50 55 60
 Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
 65 70 75 80
 Cys Ala

<210> 283
 <211> 80
 <212> PPT
 <213> Conus geographus

<210>
 <211> SITE
 <212> (1)..(30)
 <213> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at re-
 sidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues
 24 and 28 may be Trp or bromo-Trp

<400> 283
 Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile
 1 5 10 15
 Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
 20 25 30

<210> 284
 <211> 318
 <212> DNA
 <213> Conus textile

<210>
 <211> CDS
 <212> (3)..(164)

<210>
 <211> misc_feature
 <212> (1)..(318)
 <213> n may be any nucleotide

<400> 284
 gc tgc agg tgg act cta gag ggg ttg gag aat ctt tat ctg aag gca 47
 Cys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala
 1 5 10 15
 ca' cat gaa atg aac aac ccc gaa gac tct gaa ttg aac aag agg tgc 95
 His His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys
 20 25 30

t g c a t t t t c g t c t g c c t c t a a a a c t g c c g t g a t g t c t t c t a c t c c c t 194
 t a p c y s f l e p h e v a l c y s l e u
 (3)

cggtgtatgc tacctggctt gatctttgat tggcggctgc ccttcaactgg ttatgaaccc 254

crat atctcg actctctggg ggctctgggg atccaacatc aaaatanagc gacagcacia 314

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0010: 005
0011: 04
0012: FBI
0013: Census textile

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100-115
Tyr Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala His
 5 10 15

His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys Tyr
20 25 30

Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp
35 40 45

Cys Ile Phe Val Cys Leu
6)

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0010 : 36
0011 : 34
0012 : FFT
0013 : Corpus textile

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120 SITE
121 (1)..(24)
122 Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
123 O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
    bromo-Trp

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1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
 Cys Met Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
 1 5 10 15

Arg Asa Cys Ile Phe Val Cys Leu
29

010	187
011	480
012	70A
013	<i>Quercus quercinus</i>

001 - 003
 001 - (1,2) ... (333)

400 - 267
jetttgttatt tctctgtgt ctctcttggc atcaccacaa acatcaccaa g atg aaa 57
Met Lys
1

ctg arg tgc atg atg atc gtt gct ctg ctg ttc ttg acc gcc tgg aca 105
 Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala Trp Thr
 5 10 15

ttc ttc arg gct gtt gac tcc aaa aat gaa ctg gag aac aga gga gga 153
 Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg Gly Gly
 20 25 30

tgg ggg cag gca gga gga tgg ggg aaa ctt ttt cgg atg gca cgc gac 201
 Tyr Gly Gln Ala Gly Gly Trp Gly Lys Leu Phe Pro Met Ala Arg Asp
 35 40 45 50

gaa atg aaa aac agc gaa gtc tct aaa ttg gac aat aag aga aag tgc 249
 Glu Met Lys Asn Ser Glu Val Ser Lys Leu Asp Asn Lys Arg Lys Cys
 55 60 65

cct gaa gac ggt gaa gct tgc gta ata cct atc att gga aac gta ttt 297
 Ala Ala Ala Gly Glu Ala Cys Val Ile Pro Ile Ile Gly Asn Val Phe
 70 75 80

tgg tgc aaa ggc tac tgt ctt ttc gtc tgc att agt taaactgctg 343
 Cys Cys Lys Gly Tyr Cys Leu Phe Val Cys Ile Ser
 85 90

tttgacctt tactcaacct tgtgtacct ggttgatct ttgattggca tgtgcccttc 403
 aatgattat agctgtgtg atctactct ctggagacct ctgtggtcca acatccaaat 463
 aaacaggaat cccaatg 480

1210- 128
 1211- 24
 1212- PBT
 1213- Conus quercinus

1210- 1288
 Met Lys Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg
 20 25 30

Gly Gly Trp Gly Gln Ala Gly Gly Trp Gly Lys Leu Phe Pro Met Ala
 35 40 45

Arg Asp Glu Met Lys Asn Ser Glu Val Ser Lys Leu Asp Asn Lys Arg
 50 55 60

Lys Cys Ala Ala Ala Gly Glu Ala Cys Val Ile Pro Ile Ile Gly Asn
 65 70 75 80

Val Phe Cys Cys Lys Gly Tyr Cys Leu Phe Val Cys Ile Ser
 85 90

1210- 1289
 1211- 24
 1212- PBT
 1213- Conus quercinus

1210-
 1211- SITE
 1212- (1) .. (29)
 1213- Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 11 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Tyr, 125-I

-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

4400- 291

Cys Ala Ala Ala Gly Xaa Ala Cys Val Ile Xaa Ile Ile Gly Asn Val
1 5 10 15

Ile Cys Cys Lys Gly Xaa Cys Leu Phe Val Cys Ile Ser
20 25

4410- 390

4411- 410

4412- DNA

4413- *Canus leopardus*

4420-

4421- GDS

4422- (12..(246)

4430- 291

ata aaa atg atg tgc gtg gtg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

ata ata ttc atc atg gct gat gac tcc aca aat gga ctg gag aat cgt 96
Tyr Ile Phe Ile Thr Ala Asp Asp Ser Thr Asn Gly Leu Glu Asn Arg
20 25 30

ttt agg aag gca cgt gac aac atg aag aac gcc aaa gcc tct aca tta 144
Phe Arg Lys Ala Arg Asp Asn Met Lys Asn Ala Lys Ala Ser Thr Leu
35 40 45

atg gag aag aaa gag tgt gtt gaa ctt ggt gag att tgt gcc aca ggc 192
Ala Glu Lys Lys Ala Cys Val Glu Leu Gly Glu Ile Cys Ala Thr Gly
50 55 60

atc ttc cta gac gag gaa tgc tgc act ggt tca tgc cat gtc ttc tgc 240
Ile Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys
65 70 75 80

ata ata tagttaaaact gctgtgatgt cttattctct cctcgtgtgt acctggcttg 296
Met Leu

atcttgatt ggtgcctgac ctccagtggt tgtgaaaccc tatgatccta ctctctggac 356

gctctgagg cccaacatcc aaataaagcg acatcctaata ggcacacacac aaaa 410

4410- 291

4411- 390

4412- 451

4413- *Canus leopardus*

4430- 291

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Ile Ile Phe Ile Thr Ala Asp Asp Ser Thr Asn Gly Leu Glu Asn Arg
20 25 30

Ile Arg Lys Ala Arg Asp Asn Met Lys Asn Ala Lys Ala Ser Thr Leu
35 40 45

Ala Glu Lys Lys Ala Cys Val Glu Leu Gly Glu Ile Cys Ala Thr Gly
50 55 60

Phe Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys
 (1) 70 75 30

Val Leu

01000 242

0110 30

0110 FFT

0110 Conus leopardus

0110

0110 SITE

0110 11... (30)

0110 Xaa at residues 4, 7, 17 and 18 may be Glu or gamma-carboxy-Glu.

01000 242

Ala Cys Val Xaa Leu Gly Xaa Ile Cys Ala Thr Gly Phe Phe Leu Asp
 1 5 10 15

Xaa Xaa Cys Cys Thr Gly Ser Cys His Val Phe Cys Val Leu
 20 25 30

01000 242

0110 30

0110 DCA

0110 Conus marmoreus

01000

0110 CTS

0110 11... (231)

01000 242

atg aaa atg aag tgc gtg gtg atc gtt gct gtg atg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

atg aca ttt gcc aag gct gat gac gcc aga aat gga ttg gag aat ctt 96
 Tyr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30

atc tgc aag gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

aac aag aag tgc cct aac act ggt gaa tta tgt gat gtg gtt gaa caa 192
 Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
 50 55 60

aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta taaaactacc 241
 Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
 65 70 75

atgaatgtctt ctactccct ctgtgctgcc tggcttgatc ttgattggc gcgtgccctt 301

atgtgttat gaccccttg atccgacctc tgggg 336

01000 244

0110 30

0110 FFT

0110 Conus marmoreus

01000 244

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala

1	5	10	15
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu			
	20	25	30
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu			
	35	40	45
Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln			
	50	55	60
Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu			
	65	70	75

1100 295

1110 300

1120 305

1130 Calus marmoreus

1140

1150 SITE

1160 (11) (16)

1170 Xaa at residue 3 may be Pro or hydroxy-Pro; Xaa at residues 6 and 11 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

1180 195

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys			
	5	10	15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu	
	20 25

1190 196

1200 197

1210 198

1220 Sinus quercinus

1230

1240 CDS

1250 (2) (240)

1260 200

ggtacc atg aaa ctg acg tgt atg ggg atc gtt gct gtg cta ttc ttg	48
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu	
	1 5 10

acc gcc tgg gct gat gac tcc aga aat gga ttc gag aat cga aat gga	96
Thr Ala Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly	
	15 20 25 30

aaa cga aac gaa aac gaa atg aag aac ctc gaa gcc tct aaa ttg aac	144
Glu Arg Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn	
	35 40 45

aaa aga gac ggc gat tcc gtt gat ggt ggt gaa ttt tgt ggc ttt ccg	192
Arg Arg Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro	
	50 55 60

aaa att gga ggg cca tgc tgt agt ggc tgg tgc ttt ttc gtc tgc tta	240
Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu	
	65 70 75

tttactgtac atgatgtctt ctacccccct ctgtgtctacc tgacttgatc ttgattggc 300
 gttttccctt cactgggttat gaacccctct gatccgactc tctggaggcc tcgggggtcc 360
 aatatacaca taaagcgaca gcaaaaaaaa aaaaaaaaaa aa 402

210 287
 211 78
 212 FFT
 213 Conus quercinus

240 287
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly Glu Arg
 20 25 30
 Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn Arg Arg
 35 40 45
 Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro Lys Ile
 50 55 60
 Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
 65 70 75

210 298
 211 38
 212 FFT
 213 Conus quercinus

220
 221 SITE
 222 (1)..(10)
 223 Xaa at residue 9 may be Glu or gamma-carboxy-Glu; Xaa at residues
 14 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp
 or bromo-Trp

240 293
 Asp Gly Asp Cys Val Asp Gly Gly Xaa Phe Cys Gly Phe Xaa Lys Ile
 1 5 10 15
 Gly Gly Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu
 20 25 30

210 299
 211 274
 212 DNA
 213 Conus quercinus

220
 221 CDS
 222 (7)..(216)

230
 231 misc_feature
 232 (1)..(274)
 233 n may be any nucleotide

240 299
 ggatccc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg cta ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acc gac ttg gct gat gac tcc aga aat gga ttg gag aat cga aat gaa 96
 Thr Ala Leu Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Arg Asn Glu
 15 20 25 30

caa gaa gga aac gaa aac gaa atg agg gac cgc cgg gac tgc caa gat 144
 Gln Glu Arg Asn Glu Asn Glu Met Arg Asp Arg Arg Asp Cys Gln Asp
 35 40 45

act ggt ata gtt tgt ggc ttt ccg aaa cct gaa cca cac tgc tgc agt 192
 Ser Gly Val Val Cys Gly Phe Pro Lys Pro Glu Pro His Cys Cys Ser
 50 55 60

gag tgg tgc ctt ttc gtc tgc gcc taaaactgcc gtgatgtcaa ataaagcgac 246
 Gly Trp Cys Leu Phe Val Cys Ala
 65 70

agcgaatnna aaaaaaaaaa aaaaaaaaaa 274

110- 300

111- 78

112- FFT

113- Conus quercinus

140- 300

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 5 10 15

Leu Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Arg Asn Glu Gln Glu
 20 25 30

Arg Asn Glu Asn Glu Met Arg Asp Arg Arg Asp Cys Gln Asp Ser Gly
 35 40 45

Val Val Cys Gly Phe Pro Lys Pro Glu Pro His Cys Cys Ser Gly Trp
 50 55 60

Cys Leu Phe Val Cys Ala
 65 70

110- 301

111- 28

112- FFT

113- Conus quercinus

110-

111- SITE

112- (1)..(28)

113- Xaa at residues 12, 14 and 16 may be Pro or hydroxy-Pro; Xaa at r
 esidue 15 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may b
 e Trp or bromo-Trp

140- 301

Asp Cys Gln Asp Ser Gly Val Val Cys Gly Phe Xaa Lys Xaa Xaa Xaa
 5 10 15

Glu Cys Cys Ser Gly Xaa Cys Leu Phe Val Cys Ala
 20 25

110- 302

111- 340

112- ICMA

113- Conus arenatus

120-

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 <122> (7)..(246)

<120>
 <121> misc_feature
 <122> (1)..(340)
 <123> n may be any nucleotide

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 1 5 10
 aac acc tgg aca ttc gtc acg gct gac tcc ata cgt gca ctg gag gat 96
 Thr Ala Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp
 15 20 25 30
 ttc att gag aag gca cgt gac gaa atg gaa aac agc gga gct tct cca 144
 Phe Phe Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro
 35 40 45
 ttr aac gag aga gac tgc cga cct gta ggt caa tat tgt ggc ata ccg 192
 Leu Asn Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro
 50 55 60
 tat aag cac aac tgg cga tgc tgc agt cag att tgt gca att atc tgt 240
 Tyr Lys His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys
 65 70 75
 gac acc taacccctct gatccactc tctgaagacc tccgggattc aacatccaaa 296
 Val Ser
 80
 taaagcgaca tcccgatnaa aaaaaaargaa aaaaaaaaaa aaaa 340

<110> 303
 <111> 80
 <112> EST
 <113> *Corvus arenatus*

<400> 303
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp Phe Phe
 20 25 30
 Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro Leu Asn
 35 40 45
 Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro Tyr Lys
 50 55 60
 His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
 65 70 75 80

<110> 304
 <111> 80
 <112> EST
 <113> *Corvus arenatus*

<120>
 <121> SITE
 <122> (1)..(30)

4220: Xaa at residues 4 and 12 may be Pro or hydroxy-Pro; Xaa at residues 8 and 13 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 17 may be Trp or bromo-Trp

4400: 304

Asp Cys Arg Xaa Val Gly Gln Xaa Cys Gly Ile Xaa Xaa Lys His Asn
1 5 10 15

Xaa Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
20 25 30

4210: 305

4211: 381

4212: DNA

4213: *Conus arenatus*

4220:

4221: CDS

4222: (7)..(334)

4400: 305

ggatccc atg aaa ctg acg tgt gtg gtg atc gtt gtt gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttc gtc aag gct gat gac tcc ata aat gga ttg gag 96
Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu
15 20 25 30

aac ctt ttt ccc aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ttg aac gag agg tgc ctt gaa aag ggt gta ctt tgt gat ccg agt 192
Lys Leu Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser
50 55 60

ggt gga aac tgc tgt agt ggc gaa tgc gtt tta gtc tgc ctc 234
Ala Gly Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu
65 70 75

caaaactacc gtgatgtctt ctactcccat ctgtgtacc cctcgag 281

4410: 306

4411: 76

4412: PET

4413: *Conus arenatus*

4400: 306

Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser Ala Gly
50 55 60

Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu
65 70 75

0100 307
 0110 25
 0120 PPT
 0130 Conus arenatus

0200
 0210 SITE
 0220 (1)..(25)
 0230 Xaa at residues 3 and 19 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 10 may be Pro or hydroxy-Pro

0400 307
 Cys Leu Xaa Lys Gly Val Leu Cys Asp Xaa Ser Ala Gly Asn Cys Cys
 1 5 10 15
 Ser Gly Xaa Cys Val Leu Val Cys Leu
 20 25

0100 308
 0110 287
 0120 DNA
 0130 Conus arenatus

0200
 0210 CBS
 0220 (7)..(240)

0400 308
 ggaatc atg aaa ctg acg tgc atg gtg atc gtt act gtg ttg ttc ttg 48
 Met Lys Leu Thr Cys Met Val Ile Val Thr Val Leu Phe Leu
 1 5 10
 44c gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gaa ttg gag 96
 Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu
 15 20 25 30
 aat ctt ttt ctg aag gca tat cac gaa atg aac tcc gaa gcc tct aaa 144
 Asn Leu Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys
 35 40 45
 ttg gac aag aaa gag tgc gtt gct ggt agt cac ttt tgt ggt ttt ccg 192
 Leu Asp Lys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro
 50 55 60
 aaa att gga ggg cca tgc tgc agt ggc tgg tgc ttt ttc gtc tgc ttg 240
 Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
 65 70 75
 aaaaacctgcc gtgatgtctt ctactcccat ctgtgctacc cctcgag 287

0100 309
 0110 78
 0120 PPT
 0130 Conus arenatus

0400 309
 Lys Leu Thr Cys Met Val Ile Val Thr Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu Asn Leu
 20 25 30
 Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys Leu Asp
 35 40 45

Lys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro Lys Ile
 50 55 60

Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
 65 70 75

110 310
 111 28
 112 PFT
 113 Conus arenatus

120
 121 SITE
 122 (1)..(28)
 123 Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residues
 11 and 17 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Tr
 p or bromo-Trp

400 310
 Xaa Cys Val Ala Gly Ser His Phe Cys Gly Phe Xaa Lys Ile Gly Gly
 5 10 15

Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu
 20 25

110 311
 111 400
 112 DNA
 113 Conus tessulatus

120
 121 CDS
 122 (7)..(243)

400 311
 gaaac atg aaa ctg acg tgt gtg gtg atc gtt gct gtg atg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu
 1 5 10

acc gcc tgg aca ttc atc acg gct gat gac tcc ata aat gga ctg gag 96
 Thr Ala Trp Thr Phe Ile Thr Ala Asp Asp Ser ile Asn Gly Leu Glu
 15 20 25 30

gat aga ggc ata tgg ggg gaa cct ttg tgg aag gca cgt gac gaa atg 144
 Asp Arg Gly ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met
 35 40 45

aac ccc gaa gtc tct aaa cgg gat tgc tgg cct caa tat tgg ttt tgt 192
 Asn Pro Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys
 50 55 60

agg cta cag agg gga tgc tgc cca ggg act act tgc ttc ttc ctt tgc 240
 Gly Leu Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys
 65 70 75

tta tagtgatctc ttcaactccc ttctgtgcta cctggcttga cctttgattg 293
 Phe

agpctgccc ttcaactgggt ataaacccct ctgttctctc ttcttggaag cttcgggggtg 353

agagcatcc aaataaagg acgtccccc aaaaaaaaa aaaaaaa 400

110 312

<211> 79
 <212> PRT
 <213> Conus tessulatus

<400> 312
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Ile Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asp Arg
 20 25 30
 Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met Asn Pro
 35 40 45
 Gln Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys Gly Leu
 50 55 60
 Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys Phe
 65 70 75

<210> 313
 <211> 26
 <212> PRT
 <213> Conus tessulatus

<400>
 <211> SITE
 <212> (1)..(26)
 <213> Xaa at residues 3 and 7 may be Trp or bromo-Trp; Xaa at residues
 4 and 17 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Tyr,
 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
 -Tyr

<400> 313
 Asp Cys Xaa Xaa Gln Xaa Xaa Phe Cys Gly Leu Gln Arg Gly Cys Cys
 1 5 10 15
 Xaa Gly Thr Thr Cys Phe Phe Leu Cys Phe
 20 25

<210> 314
 <211> 419
 <212> DNA
 <213> Conus tessulatus

<400>
 <211> CDS
 <212> (7)..(249)

<400> 314
 gaaac atg aaa ctg acg tgc gtg gtg gtc gtt gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Val Ala Val Leu Phe Leu
 1 5 10
 aac gcc tgg aca ttc gcc acg gct gtt gac tcc aaa cat gca ctg gcg 96
 Asn Ala Trp Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala
 15 20 25 30
 aat ctt ttt atg aag gca cgt gac gaa atg tat aac ccc gat gcc act 144
 Lys Leu Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr
 35 40 45
 aat ttg gat gat aag aga tgg tgc gct tta gat ggt gaa ctt tgt atc 192
 Lys Leu Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile

50 55 60
 ata cgg gtc att ggg tcc ata ttt tgc tgc cat ggc ata tgt atg atc 240
 Ile Phe Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile
 65 70 75
 tag ttc gtc tagttgaact gcggtgatgt cttctactcc cctctgtgct 289
 Tyr Cys Val
 80
 accctcgggtt tgatctttga ttgcctgtg ccttccactg attatgaatc cctctgatcc 349
 thrctcttga agacctcttg ggtccaaca tccaaataaa gcgacatccc aaaaaaaaaa 409
 aaaaaaaaaa 419
 4210- 315
 4211- 81
 4212- PFT
 4213- *Conus tessulatus*
 4400- 315
 Met Lys Leu Thr Cys Val Val Val Val Ala Val Leu Phe Leu Asn Ala
 1 5 10 15
 Tyr Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala Lys Leu
 20 25 30
 Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr Lys Leu
 35 40 45
 Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile Ile Pro
 50 55 60
 Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile Tyr Cys
 65 70 75 80
 Val
 4210- 316
 4211- 19
 4212- PFT
 4213- *Conus tessulatus*
 4214-
 4215- SITE
 4216- (1)..(29)
 4217- Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
 + Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Pro or hydro
 xy-Pro; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, d
 i-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
 4400- 316
 Xaa Cys Ala Leu Asp Gly Xaa Leu Cys Ile Ile Xaa Val Ile Gly Ser
 1 5 10 15
 Ile Phe Cys Cys His Gly Ile Cys Met Ile Xaa Cys Val
 20 25
 4210- 317
 4211- 498
 4212- DNA
 4213- *Conus imperialis*

<120>
 <121> CDS
 <122> (7)..(240)

<400> 317
 ggttcc atg aaa ctg acg tgc gtg gtg ttc gtt gct gtg ccg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Phe Val Ala Val Pro Phe Leu
 1 5 10
 acg gcc tgc gta ttc atc acg gct gat gac tcc aga aat gga atc gag 96
 Thr Ala Ser Val Phe Ile Thr Ala Asp Asp Ser Arg Asn Gly Ile Glu
 15 20 25 30
 aat ttt cct cgg atg aga cgt cac gaa atg aag aac ccc aaa gcc tct 144
 Asn Leu Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser
 35 40 45
 aca ttg aac aag aga cag tgc cgt gta gaa ggt gaa att tgt ggc atg 192
 Lys Leu Asn Lys Arg Gln Cys Arg Val Glu Gly Glu Ile Cys Gly Met
 50 55 60
 cgg ttt gaa gca caa tgc tgc gat ggc tgg tgc ttt ttc gtc tgc atg 240
 Leu Phe Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met
 65 70 75
 taaactgcc gtgatgtctt ctactctctt ctgtgctacc tgccttgatc ttgattggc 300
 tggggccctt cattgggttat gaacccctct gatcctactc tctggaggcc tcaggggtcc 360
 agcatctaaa taaagcgaca tcacaatcaa aaaaaaaaaa aaaaaaaaaa 408

<120> 318
 <121> 75
 <122> PRT
 <123> Conus imperialis

<400> 318
 Met Lys Leu Thr Cys Val Val Phe Val Ala Val Pro Phe Leu Thr Ala
 1 5 10 15
 Ser Val Phe Ile Thr Ala Asp Asp Ser Arg Asn Gly Ile Glu Asn Leu
 20 25 30
 Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Gln Cys Arg Val Glu Gly Glu Ile Cys Gly Met Leu Phe
 50 55 60
 Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met
 65 70 75

<120> 319
 <121> 27
 <122> PRT
 <123> Conus imperialis

<120>
 <121> SITE
 <122> (1)..(27)
 <123> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 5, 7 and
 14 may be Glu or gamma-carboxy-Glu; Xaa at residue 21 may be Trp
 or bromo-Trp

0400 313
 Xaa Cys Arg Val Xaa Gly Xaa Ile Cys Gly Met Leu Phe Xaa Ala Gln
 1 5 10 15

Cys Cys Asp Gly Xaa Cys Phe Phe Val Cys Met
 20 25

0410 320
 0411 291
 0412 DGA
 0413 Genus characteristic

0420
 0421 CDS
 0422 (7)..(234)

0430 320
 agatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acc acc tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag 96
 Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu
 15 20 25 30

aac att ttt cag aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
 35 40 45

aaa ctg aac aag agg tgc gtt gac cct ggt gaa ttt tgt ggt ccg gga 192
 Lys Leu Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly
 50 55 60

ttt gga gat tgc tgc act ggc ttc tgc att tta gtc tgc atc 234
 Phe Gly Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
 65 70 75

taaaactgac gtgatgtctt ctactcccat ctgtgctaac cctcgag 281

0440 321
 0441 76
 0442 FFT
 0443 Genus characteristic

0450 321
 Cys Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly Phe Gly
 50 55 60

Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
 65 70 75

0460 322
 0461 36
 0462 FFT
 0463 Genus characteristic

1120-
 1121- SITE
 1122- (1)..(25)
 1123- Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residue
 6 may be Glu or gamma-carboxy-Glu

1100- 323
 Cys Val Asp Xaa Gly Xaa Phe Cys Gly Xaa Gly Phe Gly Asp Cys Cys
 1 5 10 15
 Thr Gly Phe Cys Leu Leu Val Cys Ile
 20 25

1110- 323
 1111- 327
 1112- DNA
 1113- Conus miliaris

1120-
 1121- CDS
 1122- (7)..(240)

1100- 323
 atacc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ttg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10
 acc ggc tgg aga ttc gtc atg gct gat gac tcc aga aat gat ttg gag 96
 Thr Ala Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu
 15 20 25 30
 att ctt ttt ctg aag gca cgt cat gaa atg aag aac ccc gaa gct tct 144
 Asn Leu Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
 35 40 45
 aaa ttg aac aag aga tgc ctt cca aat ggt gta ctt tgt gat ctg gga 192
 Lys Leu Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly
 50 55 60
 att cca cca tac tgc tgc agt ggc tgg tgc ggc atc gtc gtc tgc atc 240
 Ser Pro Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile
 65 70 75
 caaaactgtc gtcattgtctt ctactcccat ctgtgctaac cctogag 287

1100- 324
 1110- 78
 1112- FRT
 1113- Conus miliaris

1100- 324
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu Asn Leu
 20 25 30
 Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly Ser Pro
 50 55 60
 Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile

65

70

75

0108 305
 0110 17
 0112 PFT
 0113 Conus miliaris

0200
 0211 SITE
 0222 (1)..(27)
 0223 Xaa at residues 3, 13 and 14 may be Pro or hydroxy-Pro; Xaa at residue 15 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 20 may be Trp or bromo-Trp

0400 305
 Cys Leu Xaa Asn Gly Val Leu Cys Asp Leu Gly Ser Xaa Xaa Xaa Cys
 5 10 15

Tyr Ser Gly Xaa Cys Ala Ile Val Val Cys Ile
 20 25

0119 316
 0111 297
 0112 BNA
 0113 Conus atlanticus

0200
 0211 CDS
 0222 (1)..(240)

0400 316
 agatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 5 10
 1

acc gcc tgg aca ttc gtc acg gct gat gac tcc ata aat ggg ttg gag 96
 Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu
 20 25 30
 15

aat ctt ttt ccg aag gca cgt cac gaa atg agg aaa ccc gaa gcc tot 144
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Arg Lys Pro Glu Ala Ser
 35 40 45

aga tgg aga ggg agg tgc cgt cct cgt ggt atg ttc tgt ggc ttt ccg 192
 Arg Ser Arg Gly Arg Cys Arg Pro Arg Gly Met Phe Cys Gly Phe Pro
 50 55 60

aaa cct gga cca tac tgc tgc aat ggc tgg tgc ttt ttc gtc tgc atc 240
 Lys Pro Gly Pro Tyr Cys Cys Asn Gly Trp Cys Phe Phe Val Cys Ile
 65 70 75

taaaactgac gtgatgtgtt ctactcccat ctgtgctacc cctcgag 287

0110 327
 0111 78
 0112 PFT
 0113 Conus atlanticus

0400 327
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 5 10 15
 1

Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu

110 330

0110 77
 0111 PPT
 0112 Conus lividus

0400 330
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
 50 55 60
 Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
 65 70 75

0110 331
 0111 36
 0112 PPT
 0113 Conus lividus

0110
 0111 SITE
 0112 (1)..(26)
 0113 Xaa at residue 2 may be Pro or hydroxy-Pro; Xaa at residues 6 and
 11 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 ma
 y be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
 O-phospho-Tyr

0400 371
 Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
 1 5 10 15
 Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu
 20 25

0110 331
 0111 381
 0112 DNA
 0113 Conus pulicarius

0110
 0111 CDS
 0112 (7)..(234)

0400 332
 agatcc atg aaa ctg acg tgc atg gtg atc gtt gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu
 1 5 10
 tgc gcc tgg aca ttc gtc aag gct gat gac tcc aga aat gga ttg gag 96
 Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu
 15 20 25 30
 att ctt ttt ccg aag gca cgt cac gaa atg aag aac tcc aaa gcc tct 144
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Ser Lys Asn Ser Lys Ala Ser
 35 40 45
 aa tta aac aag agg tgc gtt gaa gat ggt gat ttt tgt ggt ccg gga 192
 Lys Leu Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly

50 55 60
 tat gaa gag tgc tgc agt ggc ttc tgc ctt tac gtc tgc atc 234
 Tyr Glu Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile
 65 70 75
 taaaactgac gtgatgtctt ctactcccat ctgtgctacc cctcgag 281
 01100 333
 01110 76
 01120 FFT
 01130 *Conus pulicarius*
 04000 333
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly Tyr Glu
 50 55 60
 Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile
 65 70 75
 01100 334
 01110 28
 01120 FFT
 01130 *Conus pulicarius*
 02000
 02010 SITE
 02020 (1)...(25)
 02030 Xaa at residues 3, 13 and 14 may be Glu or gamma-carboxy-Glu; Xaa
 at residue 10 may be Pro or hydroxy-Pro; Xaa at residues 12 and
 22 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Ty
 r or O-phospho-Tyr
 04000 334
 Lys Val Xaa Asp Gly Asp Phe Cys Gly Xaa Gly Xaa Xaa Xaa Cys Cys
 1 5 10 15
 Ser Gly Phe Cys Leu Xaa Val Cys Ile
 20 25
 02100 335
 02110 293
 02120 BHA
 02130 *Conus generalis*
 03200
 03210 CDS
 03220 (1)...(249)
 04000 335
 agtatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg cta ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10
 acc gcc tgg aca ttc gtc acg gct gat gac acc aga tat aaa ctg gag 96

Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu
 15 20 25 30
 aat cct ttt ctg aag gca cgc aac gaa ctg cag aaa cac gaa gcc tct 144
 Asn Pro Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser
 35 40 45
 gaa ctg aac gag aga ggc tgc ctt gac cca ggt tac ttc tgt ggg acg 192
 Gln Leu Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr
 50 55 60
 cag ttt ctt gga gca tac tgc tgc ggt ggc att tgc ctt att gtc tgc 240
 Pro Phe Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys
 65 70 75
 ata gaa acg taaagcttg atgtcttcta ctccatctg tgctacccct ctag 293
 Ile Glu Thr
 80

210 336
 211 81
 212 PBT
 213 Conus generalis

400 336
 Met Cys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu Asn Pro
 20 25 30

Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser Gln Leu
 35 40 45

Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr Pro Phe
 50 55 60

Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Glu
 65 70 75 80

Thr

210 337
 211 30
 212 PBT
 213 Conus generalis

220
 221 SITE
 222 (1)..
 223 Xaa at residues 5 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

400 337
 Gly Cys Leu Asp Xaa Gly Xaa Phe Cys Gly Thr Xaa Phe Leu Gly Ala
 1 5 10 15

Xaa Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Xaa Thr
 20 25 30

210 338
 211 400
 212 DNA

0113- *Conus episcopatus*

0114-

0115- CDS

0116- (7)...(234)

0400- 338

atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 96
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly
15 20 25 30

acc ttt ttt tgg aat gta cat cac gaa atg aag aac ctg gaa gac tct 144
Asn Leu Phe Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser
35 40 45

aaa ttg aac aag aag tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt 192
Lys Leu Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu
50 55 60

att tca gac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta 234
Tyr Ser Asp Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

taaaactacc gtagcgtctt ctactccct ctgtgctacc tggcttgatc ttgattggc 294

gtgtgcgctt cactgggttat gaacccctct gatctactc tctgaagacc tctggggctc 354

acatccaaa taaagcgaca tcacaaaaaa aaaaaaaaaa aaaaaa 400

0118- 139

0119- 76

0120- PRT

0121- *Conus episcopatus*

0400- 339

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser Lys Leu
35 40 45

Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
50 55 60

Asp Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

0120- 140

0121- 26

0122- PRT

0123- *Conus episcopatus*

0120-

0121- SITE

0122- (1)...(25)

0123- Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residues
12 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s

ulpho-Tyr or O-phospho-Tyr

<400> 340

Cys Leu Gly Phe Gly Xaa Ala Cys Leu Met Leu Xaa Ser Asp Cys Cys
 1 5 10 15

Ser Xaa Cys Val Ala Leu Val Cys Leu
 20 25

<210> 341

<211> 404

<212> DNA

<213> *Conus episcopatus*

<220>

<221> CDS

<222> (7)...(240)

<400> 341

agatcc atg aaa ctg acg tgc gtg gtg atc att gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu
 1 5 10

acc gcc tag aca ttc gtc atg gct gat gac ccc aga gat gaa ccg gag 96
 Thr Ala Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu
 15 20 25 30

gga cgt gac gaa atg aac ccc gca gcc tct aaa ttg aac gag aga ggc 144
 Ala Arg Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly
 35 40 45

tgc ctt gca gtt gat tat ttt tgc gcc ata ccg ttt gtg agc aac ggc 192
 Cys Leu Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly
 50 55 60

cta tgc tgc agt ggc aat tgt gtt ttt gtc tgc aca ccc caa ggc aag 240
 Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
 65 70 75

taaaaactgcc gtgacgtctt ctactccct ctgtgctacc tggcttgatc ttgattggc 300

ggtgacactt cactgggttat gaacccctct gatcctactc tctgaagacc tctgggggtcc 360

acatccaaa taaagcgaca tcccaaaaaa aaaaaaaaaa aaaa 404

<210> 340

<211> 78

<212> FFT

<213> *Conus episcopatus*

<400> 342

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg
 20 25 30

Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
 35 40 45

Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly Leu Cys
 50 55 60

Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys

65

70

75

4010 343
 4011 31
 4012 PFT
 4013 Conus episcopatulus

4020
 4021 SITE
 4022 (1)..(31)
 4023 Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydroxy-Pro

4030 342
 Gly Cys Leu Ala Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Ser Asn
 1 5 10 15
 Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
 20 25 30

4040 344
 4041 192
 4042 DNA
 4043 Conus achatinus

4050
 4051 CDS
 4052 (85)..(171)

4060 344
 agatcctctg tctccatct attattatct gctgcaaac tgtgttaaatt attcaagtct 60
 ctcttctctg ttgtgtctaa cagg ttg aga tgg tgc att cct aga ggt gat 111
 Leu Arg Trp Cys Ile Pro Arg Gly Asp
 1 5
 att tgt ttc ccc tgc gat cgc ata caa tgc tgc agt ggc aag tgc aca 159
 Leu Cys Phe Pro Ser Asp Arg Ile Gln Cys Cys Ser Gly Lys Cys Thr
 10 15 20 25
 ctg tgc tgc atg taaaactgcc gtgatgtctt ctctccct c 202
 Phe Val Cys Met

4070 345
 4071 19
 4072 PFT
 4073 Conus achatinus

4080 345
 Leu Arg Trp Cys Ile Pro Arg Gly Asp Leu Cys Phe Pro Ser Asp Arg
 1 5 10 15
 Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
 20 25

4090 346
 4091 17
 4092 PFT
 4093 Conus achatinus

4100
 4101 SITE
 4102 (1)..(27)

1120 Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 11 may be Pro or hydroxy-Pro

1400 346

Xaa Cys Ile Xaa Arg Gly Asp Leu Cys Phe Xaa Ser Asp Arg Ile Gln
1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

1120 347

111 300

112 DNA

113 Genus achatinus

1120

111 CDS

112 (35)..(171)

1400 347

tgatctcttg tctctctctt tcattcattc gctgcacaaac tgtattaaat attcgaatct 60

ctctctctct ttgtgtctga caga ttg aga ggg tgc gtt cct agt ggt gaa 111
Leu Arg Gly Cys Val Pro Ser Gly Glu
1 5

agt tgt tac ttc atg gat cac ata gga tgc tgc agt ggc aag tgc aca 159
Ile Cys Tyr Phe Met Asp His Ile Gly Cys Cys Ser Gly Lys Cys Thr
10 15 20 25

ctc gtc tgc atg taaaactgcc gtgatgtctt ctctctccat c 202
Ile Val Cys Met

1110 348

111 29

112 PFT

113 Genus achatinus

1400 348

Leu Arg Gly Cys Val Pro Ser Gly Glu Ile Cys Tyr Phe Met Asp His
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

1110 349

111 27

112 PFT

113 Genus achatinus

1400

111 SITE

112 (1)..(27)

113 Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

1400 349

Gly Cys Val Xaa Ser Gly Xaa Ile Cys Xaa Phe Met Asp His Ile Gly
1 5 10 15

Lys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

0210 350
 0211 264
 0212 DNA
 0213 Conus bullatus

0220
 0221 SITE
 0222 (1)..(234)

0400 350
 atg aaa atg acg tgc gtg atg atc gtt act gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
 1 5 10 15
 atg aca ttc gtc acg gct gat gac tcc aca tat gga ttg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Thr Tyr Gly Leu Lys Asn Leu
 20 25 30
 atg atg aac gga cgt cat gaa atg atg aac ccc gaa gcc cct aaa ttg 144
 Met Pro Asn Gly Arg His Glu Met Met Asn Pro Glu Ala Pro Lys Leu
 35 40 45
 aac aag aaa gat gaa tgc tct gct cct ggt gca ttt tgt ctc atc agg 192
 Asn Lys Lys Asp Glu Cys Ser Ala Pro Gly Ala Phe Cys Leu Ile Arg
 50 55 60
 aca aga ctc tgc tgc agc gag ttc tgc ttc ttt gcg tpt ttt 234
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Phe Ala Cys Phe
 65 70 75
 taatgacggt tgatgtcttc taatcccttc 264

0210 351
 0211 78
 0212 PPT
 0213 Conus bullatus

0400 351
 Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
 1 5 10 15
 tip thr phe val thr ala asp asp ser thr tyr gly leu lys asn leu
 20 25 30
 leu pro asn gly arg his glu met met asn pro glu ala pro lys leu
 35 40 45
 asn lys lys asp glu cys ser ala pro gly ala phe cys leu ile arg
 50 55 60
 pro gly leu cys cys ser glu phe cys phe phe ala cys phe
 65 70 75

0210 352
 0211 27
 0212 PPT
 0213 Conus bullatus

0220
 0221 SITE
 0222 (1)..(27)
 0223 Xaa at residues 2 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residues 6 and 14 may be Pro or hydroxy-Pro

4400 352

Asp Xaa Cys Ser Ala Xaa Gly Ala Phe Cys Leu Ile Arg Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Phe Ala Cys Phe
20 25

4410 353

4411 276

4412 DNA

4413 Conus bullatus

4420

4421 CDS

4422 (1)..(246)

4400 353

atg aaa ctg acg tgc gtg atg atc gtt act gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga gac gct ccg gat agt gca 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala
20 25 30

gaa aga tgg gag aaa ctt ttc tgc gag gaa cgt gac gaa atg aag aac 144
Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn
35 40 45

acc aaa gac ttt gaa ttg aga ggg tgc ctt cct agg tgg gaa ttt tgt 192
Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys
50 55 60

ccc atc ttt aaa aaa aac gat tgc tgc agt ggc ata tgc ata agc atc 240
Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile
65 70 75 80

tgc ttg taaaactccg tgatgtcttc tottcccatc 276
Cys Leu

4410 354

4411 82

4412 FFT

4413 Conus bullatus

4400 354

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala
20 25 30

Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn
35 40 45

Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys
50 55 60

Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile
65 70 75 80

Cys Leu

4410 355

011 27
012 PPT
013 Conus bullatus

020
021 SITE
022 (1)..(27)
023 Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu

400 355
Gly Cys Leu Xaa Arg Xaa Xaa Phe Cys Xaa Ile Phe Lys Lys Asn Asp
1 5 10 15
Cys Cys Ser Gly Ile Cys Ile Ser Ile Cys Leu
20 25

010 356
011 268
012 DNA
013 Conus striolatus

020
021 GDS
022 (1)..(237)

400 356
atg aaa atg aag tgc atg atg att gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
ttg ata ttt gta atg gct gat gac tcc aga aat gga ttg gag aat ctt 96
Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30
act aag act aca cgt cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45
aac aag aca gac tgc ctt gct aaa gac gct ttc tgt gcc tgg ccg ata 192
Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile
50 55 60
ttt gga aca ctg tgc tgc agt cgc ttg tgc tta tac gtc tgc atg 237
Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
65 70 75
taaaactgcc gtgatgtctt ctactccct 2 268

010 357
011 79
012 PPT
013 Conus striolatus

400 357
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30
Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile
50 55 60

Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
65 70 75

0110 - 358
0111 - 18
0112 - FFT
0113 - Genus striolatus

020 -
021 - SITE
022 - (1)...(28)
023 - Xaa at residue 11 may be Trp or bromo-Trp; Xaa at residues 12 and
16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tyr, 125-
I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

0400 - 353
Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa
1 5 10 15

Leu Cys Cys Ser Arg Leu Cys Leu Xaa Val Cys Met
20 25

0110 - 359
0111 - 266
0112 - DNA
0113 - Genus consors

020 -
021 - GDS
022 - (1)...(246)

0400 - 359
Atg aaa ctg acg tgc atg atg atc gtt got gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg got gat gac tcc aga aat gga ttg gag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

tct ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tcg 144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac 192
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

gca gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

ttt tgg tgaatgtcttc tctccctc 266
Phe Ser

0110 - 360
0111 - 81
0112 - FFT
0113 - Genus consors

0400 - 360

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
 35 40 45
 Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
 50 55 60
 Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
 65 70 75 80
 Phe Ser

110 361
 111 31
 112 PPT
 113 Cons consors

110
 111 SITE
 112 (1)...(31)
 113 Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

400 361
 Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
 1 5 10 15
 Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
 10 25 30

110 362
 111 289
 112 DNA
 113 Cons consors

110
 111 CDS
 112 (1)...(252)

400 362
 atg aaa ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc acc 48
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Thr 15
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu 20 25 30
 ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 35 40 45
 1 5 10 15
 aac aag aga gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt 192
 Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg 50 55 60
 1 5 10 15
 tta gga ctc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt 240
 Phe Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe 10 15 20 25 30

65

70

75

80

gtt gat tct ggc taacagtgtg cgttggttga tgtttctac tccctc
Val Asp Ser Gly

289

-110- 362

-111- 84

-112- FFT

-113- Conus consors

-400- 363

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

Val Asp Ser Gly

-110- 364

-111- 85

-112- FFT

-113- Conus consors

-120-

-121- SITE

-122- (1)..(32)

-123- Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
Xaa at residue 25 may be Trp or bromo-Trp

-400- 364

Asp Gly Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser
20 25 30

-110- 365

-111- 205

-112- DNA

-113- Conus circumcissus

-120-

-121- GDS

-122- (83)..(175)

-400- 365

atccatct gtccatccat ctattcatto attogctgoc aaactgtatt aaatattcaa
60

gtctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10
112

gat att tgt ttc ccc tgc gat cac ata caa tgc tgc aat gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
 15 20 25

gga ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcttcctc 205
 Ala Phe Val Cys Leu
 30

4000 366
 4010 31
 4015 PRT
 4018 Genus circumcisis

4000 366
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15
 Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
 20 25 30

4010 367
 4011 26
 4015 PRT
 4018 Genus circumcisis

4000
 4011 SITE
 4012 (1)..(16)
 4013 Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

4000 367
 Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
 1 5 10 15
 Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
 20 25

4010 368
 4011 206
 4015 DNA
 4017 Genus circumcisis

4000
 4011 CFS
 4012 (13)..(175)

4000 368
 ggtacatct gtccatccat ctattcattc attcgctgtc aaactgtatt aaatattcaa 60
 ggtctctttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
 1 5 10

gat att tgt ttc ccc tgc gat cac ata caa tgc tgc agt gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
 15 20 25

gga ttc gtc tgc ttg taaaactgcc gtgatgtctt ctactccct c 206
 Ala Phe Val Cys Leu
 30

4010 369
 4011 31
 4015 PRT

<213> Conus circumcissus

<400> 369

Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25 30

<210> 370

<211> 27

<212> PRT

<213> Conus circumcissus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
1 may be Pro or hydroxy-Pro

<400> 370

Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
1 5 10 15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25

<210> 371

<211> 106

<212> DNA

<213> Conus circumcissus

<220>

<221> CDS

<222> (33)..(175)

<400> 371

ggtacatcat gtcacatcat ctattccattc attcctctgtc aaactgtatt aaatattcaa 60

gctctctctt cgttttctgt ct aac aga ttg agt agg tgc att cct agt ggt 112
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10

gat cct tgt ttc ccc tgg gat cac ata caa tgc tgc agt gcc aag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctctccct c 206
Ala Phe Val Cys Leu
30

<210> 372

<211> 31

<212> PRT

<213> Conus circumcissus

<400> 372

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25 30

<210> 373

0110 36
 0111 PPT
 0113 Genus circumciscus

0200
 0201 SITE
 0202 (1)..(26)
 0203 Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

0400 373
 Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
 1 5 10 15

Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25

0110 374
 0111 206
 0112 DNA
 0113 Genus circumciscus

0200
 0201 CDS
 0202 (83)..(175)

0400 374
 gaatcatat gtacatcat ctattcattc atttgtgtgc aaactgtatt aaatattcaa 60

atctctcttt ctgttttgt ct aac aga ttg agt agg tgc att cct agt ggt 112
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
 1 5 10

gat ctt tgt ttc ccc tgg gat cac ata xaa tgc tgc aat gcc gag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Glu Cys
 15 20 25

gaa ttc gtc tgc ttg taaaaactgcc gtgatgtctt ctctccct c 206
 Ala Phe Val Cys Leu
 30

0110 375
 0111 31
 0112 PPT
 0113 Genus circumciscus

0400 375
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Glu Cys Ala Phe Val Cys Leu
 20 25 30

0110 376
 0111 26
 0112 PPT
 0113 Genus circumciscus

0200
 0201 SITE
 0202 (1)..(26)
 0203 Xaa at residues 3 and 10 may be Pro or hydroxy-Pro; Xaa at residu
 e 20 may be Glu or gamma-carboxy-Glu

0400 376

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
 1 5 10 15

Cys Asn Ala Xaa Cys Ala Phe Val Cys Leu
 20 25

0210 - 377
 0211 - 106
 0212 - DNA
 0213 - Genus circumcisis

0220 -
 0221 - CDS
 0222 - (83)..(175)

0400 - 377
 ggaacatcat ggaacatcat ctattcatto attogctgtc aaactgtatt aaatattcaa 60
 gctctcttt cgttttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
 1 5 10
 gat ctt tgt ttc ccc tgg gat cac ata cga tgc tgc agt gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Arg Cys Cys Ser Ala Lys Cys
 15 20 25
 gaa ttc ttc tgc ttg taaaactgcc gtgatgtctt ctcttcccat c 206
 Ala Phe Val Cys Leu
 30

0210 - 378
 0211 - 11
 0212 - PFT
 0213 - Genus circumcisis

0400 - 378
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15
 Asp His Ile Arg Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25 30

0210 - 379
 0211 - 17
 0212 - PFT
 0213 - Genus circumcisis

0210 -
 0221 - SITE
 0222 - (1)..(27)
 0223 - Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
 1 may be Pro or hydroxy-Pro

0400 - 379
 Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Arg
 1 5 10 15
 Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25

0210 - 380
 0211 - 106
 0212 - DNA
 0213 - Genus circumcisis

02200
02210 CDS
02220 (#3)..(175)

04000 380
cgatccatct gtccatccat ctattcattc attcgtgtgcc aaactgtatt aaatattcaa 60
gtctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10
gat ctt tgt ttc ccc tgg gat cac ata caa tgc tgc aat gcc aag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
15 20 25
gca ttc gcc tgc ttg taaaactgcc gtgatgttt ctcttccct c 206
Ala Phe Ala Cys Leu
30

02100 381
02110 31
02120 FRT
02130 Conus circumcissus

04000 381
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15
Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
20 25 30

02100 382
02110 16
02120 FRT
02130 Conus circumcissus

02200
02210 SITE
02220 (1)..(26)
02230 Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

04000 382
Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
1 5 10 15
Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
20 25

02100 383
02110 206
02120 TNA
02130 Conus circumcissus

02200
02210 CDS
02220 (#3)..(175)

04000 383
cgatccatct gtccatccat ctattcattc attcgtgtgcc aaactgtatt aaatattcaa 60
gtctctcttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
1 5 10

gat ctt tgt ttc ccc tgc gat cac ata caa tgc tgc aat gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
 15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctactccct c 206
 Ala Phe Val Cys Leu
 30

4000 384
 4001 31
 4002 FFT
 4003 Genus circumciscus

4000 384
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15
 Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
 20 25 30

4000 385
 4001 37
 4002 FFT
 4003 Genus circumciscus

4000
 4001 SITE
 4002 (1)..(27)
 4003 Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
 1 may be Pro or hydroxy-Pro

4000 385
 Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
 1 5 10 15
 Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
 20 25

4000 386
 4001 200
 4002 DNA
 4003 Genus circumciscus

4000
 4001 CDS
 4002 (77)..(169)

4000 386
 gctactcttg tctctctota ttattattcg ctgccaaactg tattaaatat tcaagtctct 60
 tctctctgttt gtgtct aac aga ttg agt tgg tgc att cct act ggt gat ctt 112
 Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu
 1 5 10

tgt ttc ccc tgc gat cac ata caa tgc tgc agt ggc aag tgc aca ttc 160
 Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe
 15 20 25

gtc tgc atg taaaactgcc gtgatgtctt ctctctccct c 200
 Val Cys Met
 30

4000 387
 4001 31

0212: PPT
0213: *Conus circumciscus*

0400: 387
Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu Cys Phe Pro Ser
1 5 10 15
Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25 30

0210: 388
0211: 27
0212: PPT
0213: *Conus circumciscus*

0220:
0221: SITE
0222: (1)...(27)
0223: Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
1 may be Pro or hydroxy-Pro

0400: 388
Xaa Cys Ile Xaa Thr Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
1 5 10 15
Lys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

0210: 389
0211: 266
0212: DNA
0213: *Conus monachus*

0220:
0221: CDS
0222: (1)...(246)

0400: 389
atg aag atg aag tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
tgg aca ttc gtc aag gct gat gac tcc aga aat gga ttg gag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30
tct ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tgg 144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45
aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac 192
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60
gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80
ttt tgg tgaatgtttt toctccctc 266
Phe Ser

0210: 390
0211: 32
0212: PPT

0213- *Genus monachus*

0400- 390

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Pro Ser

0210- 391

0211- 31

0212- PBT

0213- *Genus monachus*

0400-

0211- SITE

0212- (1)...(31)

0213- Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

0400- 391

Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

0210- 390

0211- 277

0212- DNA

0213- *Genus stercusmuscarum*

0220-

0221- CDS

0222- (1)...(246)

0400- 392

atc aaa ctg aag tgc atg atg atc att gct gtg ctg ttc ttg aac gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc aca gct gat gac tcc ata aat tga ccg gag aat aga 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
20 25 30

gga ata tgg gag aaa ctt ttg ttg aag gca cgt gac gaa atg aag aac 144
Arg Ile Trp Glu Lys Leu Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
35 40 45

ccc gaa gcc tct caa ttg aga tgg tgc att cct agt ggt gaa ctt tgt 192
Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
50 55 60

ttc cgc tgc gat cac ata caa tgc tgc agt gcc aag tgc gca ttc gtc 240
 Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val
 65 70 75 80

tgc ttg taaaactacc gtgatgtctt ctctctccat c 277
 Cys Leu

0210 393
 0211 80
 0212 PPT
 0213 Genus stercusmuscarum

0400 393
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
 20 25 30

Arg Ile Trp Glu Lys Leu Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
 35 40 45

Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
 50 55 60

Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val
 65 70 75 80

Cys Leu

0210 394
 0211 27
 0212 PPT
 0213 Genus stercusmuscarum

0220
 0221 SITE
 0222 (1)..(27)
 0223 Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be
 Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy
 -Glu

0400 394
 Xaa Cys Ile Xaa Ser Gly Xaa Leu Cys Pro Arg Ser Asp His Ile Gln
 1 5 10 15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25

0210 395
 0211 266
 0212 DNA
 0213 Genus stercusmuscarum

0220
 0221 CDS
 0222 (1)..(246)

0400 395
 atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg atc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg aag aat ctt 96

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30
 ttt ccc aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag aga gat ggg tgc tct agt gat ggt aca ttt tgt ggc atc cgt 192
 Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
 50 55 60
 cca aga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80
 att cat tgatgtcttc tattccctc 266
 Ile Asp

110 - 396
 111 - 82
 112 - PFT
 113 - *Conus stercusmuscarum*

400 - 396
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80

Ile Asp

110 - 397
 111 - 31
 112 - PFT
 113 - *Conus stercusmuscarum*

120 -
 121 - SITE
 122 - (1) .. (31)
 123 - Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

400 - 397
 Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu
 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
 20 25 30

110 - 398
 111 - 265
 112 - PNA
 113 - *Conus striolatus*

0200
0210 CDS
0220 (1) (234)

0400 398
atg aaa atg atg tgc ata atg acc gtt gct gtg ctg ttc ttg acc gct 48
Met Lys Leu Thr Cys Ile Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
tgg aca ttc gtc atg gct gat gac tcc aga aat gga ttg gag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30
ctt atg aag aca cgt cac gaa gtg gaa aac ccc aaa ggc tct agg tgg 144
Leu Leu Lys Thr Arg His Glu Val Glu Asn Pro Lys Ala Ser Arg Ser
35 40 45
agg ggt aag tgc cgt cct ggt ggt acg gtt tgt ggc ttt cag aaa cct 192
Gly Gly Arg Cys Arg Pro Gly Gly Thr Val Cys Gly Phe Pro Lys Pro
50 55 60
gaa aca tac tgc tgc agt ggc tgg tgc ttt ttt gtc tgc gcc 234
Gly Pro Tyr Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Ala
65 70 75
ttaaactgca gtgatgttt ctctctccat c 265

0210 399
0211 78
0212 PPT
0213 Genus striolatus

0400 399
atg lys leu thr cys ile met thr val ala val leu phe leu thr ala
1 5 10 15
tgg thr phe val thr ala asp asp ser arg asn gly leu glu asn leu
20 25 30
leu leu lys thr arg his glu val glu asn pro lys ala ser arg ser
35 40 45
gly gly arg cys arg pro gly gly thr val cys gly phe pro lys pro
50 55 60
gly pro tyr cys cys ser gly trp cys phe phe val cys ala
65 70 75

0210 400
0211 17
0212 PPT
0213 Genus striolatus

0220
0230 SITE
0240 (1) (27)
0250 Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa at residue 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or brom-Trp

0400 400
cys arg xaa gly gly thr val cys gly phe xaa lys xaa gly xaa xaa
1 5 10 15

Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Ala
20 15

<210> 401
<211> 27
<212> DNA
<213> Conus striolatus

<210>
<211> CDS
<212> (1)..(243)

<400> 401
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30
ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45
gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60
acc ggg cta tgc tgc agt gag ttp tgt tta ccg gcc gtc tgc gtc ggt 240
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65 70 75 80
agt taactgccgt gatgttttct attccctc 272
Gly

<210> 401
<211> 31
<212> PFT
<213> Conus striolatus

<400> 402
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
tpp thr phe val thr ala asp asp ser lys asn gly leu glu asn his
20 25 30
phe trp lys ala arg asp glu met lys asn arg glu ala ser lys leu
35 40 45
asp lys lys glu ala cys tyr pro pro gly thr phe cys gly ile lys
50 55 60
pro gly leu cys cys ser glu leu cys leu pro ala val cys val gly
65 70 75 80
gly

<210> 403
<211> 29
<212> PFT
<213> Conus striolatus

0200

0210 SITE

0220 (1)..(29)

0230 Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be Pro or hydroxy-Pro

0400 403

Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
20 25

0210 404

0211 365

0212 DNA

0213 Conus striolatus

0210

0211 SDS

0220 (1)..(146)

0400 404

atg aaa atg acg agt atg atg gct gtt gct gtg atg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ala Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

agg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96
Arg Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

tct acg aag gca agt cac gaa atg aag aac ccc gaa gcc tct aaa tog 144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

aac aag aga tat gag tgc tat tct act ggt aca ttt agt agc atc aac 192
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

aga gga ctc tgc tgc agc aac ctt agc tta ttt ttc gtg tgc tta aca 240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

att acg tcatgtcttc tacccttc 265
Phe Ser

0210 405

0211 34

0212 PFT

0213 Conus striolatus

0400 405

Met Lys Leu Thr Cys Leu Met Ala Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Arg Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn

the Ser

1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 2680, 26

22. (1) .. (31)

· 405 · 406

Pro Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

100

(2) .. (231)

406, 407

tgt cat ctc atc acc gct gat gac tcc aga ggt acg bag aag cat cgt 96
Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ubc dtg agg tgg act acc aaa gtc tgc aag tgg act agc tgc atg aaa 144
 Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
 35 40 45

ggt ggg tct tat tgc gtc gct act acg aga atc tgc tgc ggt tat tgc 192
Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
50 55 60

ggt tat ttc ggc aaa ata tgt att ggc tat ccc aaa aac tgatcctccc 241
 Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn
 70 75

• ttttggggtt ttattctttt ttgttgtgat gttttttcct cccctc

287

. 111 . 7

113. *Conus striolatus*

405, 408

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15

Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
 35 40 45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
 50 55 60

Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn
 65 70 75

01100 409

01110 35

01120 PBT

01130 Conus striolatus

01200

01210 SITE

01220 (1)..(35)

01230 Xaa at residues 10, 21, 24 and 32 may be Tyr, 125-I-Tyr, mono-iod
 o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue
 33 may be Pro or hydroxy-Pro

04000 409

Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg
 1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Gly Xaa
 20 25 30

Xaa Lys Asn
 35